

SEQ. ID 3-1 GAAAAGGTGGACAAGTCCTATTTCAAGAGAAGATGACTTTAACAGTTGAAGGATCT 60
 SEQ. ID 4-1 M T F N S F E G S 9

61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTGAGTAGAAGAGTTAACAGA 120
 10 K T C V P A D I N K E E E F V E E F N R 29

121 TTAAAAACTTTGCTAATTTCCAAGTGGTAGTCCTGTTCAGCATCAACACTGGCACGA 180
 30 L K T F A N F P S G S P V S A S T L A R 49

181 GCAGGGTTCTTATACTGGTAAGGAGATACCGTGCGGTGCTTAGTTGTATGCAGCT 240
 50 A G F L Y T G E G D T V R C F S C H A A 69

241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300
 70 V D R W Q Y G D S A V G R H R K V S P N 89

301 TGCAAGATTTATCAACGGTTTATCTTGAAATAGTGCCACGCAGTCTACAAATTCTGGT 360
 90 C R F I N G F Y L E N S A T Q S T N S G 109

361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTGCTTA 420
 110 I Q N G Q Y K V E N Y L G S R D H F A L 129

421 GACAGGCCATCTGAGACACATGCAGACTATCTTGAGAACTGGGCAGGTGTAGATATA 480
 130 D R P S E T H A D Y L L R T G Q V V D I 149

481 TCAGACACCATAACCGAGGAACCTGCCATGTATGTAGAAAGCTAGATTAAAGTCC 540
 150 S D T I Y P R N P A M Y S E E A R L K S 169

541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCAAAGAGAGTTAGCAAGTGCTGGACTC 600
 170 F Q N W P D Y A H L T P R E L A S A G L 189

601 TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTGTTGGTGGAAAATGAAAAAT 660
 190 Y Y T G I G D Q V Q C F C C G G K L K N 209

661 TGGGAACCTTGTGATCGCTGGTCAGAACACAGGCACACTTCCTAAATTGCTTCTT 720
 210 W E P C D R A W S E H R R H F P N C F F 229

721 GTTTGGGCCGGAACTTAATATTGAAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780
 230 V L G R N L N I R S E S D A V S S D R N 249

781 TTCCCAAATTCAACAAATCTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840
 250 F P N S T N L P R N P S M A D Y E A R I 269

841 TTTACTTTGGGACATGGATATACTCAGTTAACAGGAGCAGCTGCAAGAGCTGGATT 900
 270 F T F G T W I Y S V N K E Q L A R A G F 289
 1 2

901 TATGCTTGTGAAAGGTGATAAGTAAAGTAAAGTGCCTTCAGTGTGGAGGAGGGCTAACTGAT 960
 290 Y A L G E D K V K C F H C G G G L T D 309
 2 3

961 TGGAAGCCCAGTGAAGAGCCCTGGAAACAACATGCTAAATGGTATCCAGGGTGTGCAAATAT 1020
 310 W K P S E D P W E Q H A K W Y P G C K Y 329

1021 CTGTTAGAACAGAAGGGACAAGAAATATAAACATATTCACTTAACTCATTCACTTGAG 1080
 330 L L E Q K G Q E Y I N N I H L T H S L E 349

Fig. 1

3 4 4 5

1081 GAGTGTCTGGTAAGAACTACTGAGAAAACACCATACTAAGTAGAAGAATTGATGATACC 1140
 350 E C L V R T T E K T P S L T R R I D D T 369

1141 ATCTTCAAAATCCTATGGTACAAGAAGCTATACTGAATGGGGTCAGTTCAAGGACATT 1200
 370 I F Q N P M V Q E A I R M G F S F K D I 389

1201 AAGAAAATAATGGAGGAAAAAATTCAAGATATCTGGGAGCAACTATAATCACTTGAGGTT 1260
 390 K K I M E E K I Q I S G S N Y K S L E V 409

1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAGTCAGACT 1320
 410 L V A D L V N A Q K D S M Q D E S S Q T 429

1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCCCTGCAAGAGGAGAACGTT 1380
 430 S L Q K E I S T E Q L R R L Q E E K L 449

1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTGTCCCTGGACATCTAGTC 1440
 450 C K I C M D R N I A I V F V P C G H L V 469

1441 ACTTGTAAACAATGTGCTGAAGCAGTGACAAGTGTCCCAGTGTCTACACAGTCATTACT 1500
 470 T C K Q C A E A V D K C P M C Y T V I T 489

1501 TTCAAGCAAAAATTTTATGTCTTAATCTAACTCTATAGTAGGCATGTTATGTTCT 1560
 490 F K Q K I F M S * 497

1561 TATTACCTGATTGAATGTGATGTGAACTGACTTTAACAGTAATCAGGATTGAATTCCAT 1620
 1621 TAGCATTTGCTACCAAGTAGGAAAAAAATGTACATGGCAGTTAGTTGGCAATATA 1680

1681 ATCTTGAAATTCTTGATTTCAGGGTATTAGCTGTATTATCCATTTCCTACTGT 1740

1741 TTTAATTGAAACCATAGACTAAGAATAAGAACATCATACTATAACTGAACACAATGT 1800

1801 ATTCACTAGTATCTGATTTAACCTAAAGTGTAAAGTGAATTAACTCATCTGGATTTC 1860

1861 TCTTTCAAGATAGGCTAACAAATGGAGCTTCCTGTATATAATGTGGAGATTAGGT 1920

1921 ATCTCCCCAACATCACATAATTGTTTGTGAAAAAGGAATAAATGTTCCATGCTGGT 1980

1981 GAAAGATAGAGATTGTTTAGAGGTTGGTGTGTTAGGATTCTGTCCATTTC 2040

2041 TTTAAAGTTAAACACGTACTTGTGCGAATTATTTTAAAGTGAATTGATTGCCATTTC 2100

2101 AAAGCGTATTAAATGATAGAAATACTATCGAGCCAACATGTACTGACATGGAAAGATGT 2160

2161 AAGATATGTTAAGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGAT 2220

2221 AAGTATGTATGTTTAATATGCATAGAACAAAAGATTGGAAAGATATAACCAAAC 2280

2281 TTAAATGTGGTTCTCTCGGGGAGGGGGGATTGGGGGAGGGGCCAGAGGGTTT 2340

2341 TAGGGGCCTTCACTTTCACTTTTCACTTTGTTCTGTGCAATTTCATAAGTAT 2400

2401 GTATTACTTTGTAATCAGAATTAGAAAGTATTGCTGATTTAAAGCTTAGGCAT 2460

2461 GTCAAACGCCTGCAAAACTACTTACACTCAGCTTAGTTCTAATCCAAGAAGGCA 2520

2521 GGGCAGTTAACCTTTGGTGCCTGAAATGTAAATGATTATGTTCTGCT 2580

2581 TGTGGATGAAAATATTCGAGTGGTAGTTTGTACAGGTAGACCATGTCTTATCTG 2640

2641 TTTCAAAATAAGTATTCTGATTGAAAATGAAATATAAAATGTCTCAGATCTCC 2700

2701 ATTAATTAGTAAGGATTACATCCTTAATCCTTGCTAGTTAACGCTGCCAAGTCAC 2760

2761 ACTAAAAGATCTTGTAACTCAGTATTAAACATCTGTCAGCTTATGTAGGTAAAAGT 2820

2821 AGAAGCATGTTGTACACTGCTGTAGTTATAGTGACAGCTTCCATGTTGAGATTCT 2880

2881 TATCATCTGTATCTTAAAGTTCATGTGAGTTTACCGTTAGGATGATTAAGATGT 2940

2941 ATAGGACAAAATGTTAAGTCTTCTACCTACATTGTTCTGGTAGTAATAGTA 3000

3001 GTAGATACTCTGAAATAATGTTCTCAAGATCCTTAAACCTCTGGAAATTATAAA 3060

Fig. 1 (cont.)

3061 AATATTGGCAAGAAAAGAAGAATAGTGTAAATATTTTAAAAAACACTTGAATAAG 3120
 3121 AATCAGTAGGGTATAAACTAGAAGTTAAAATGCCTCATAGAACGTCAGGGTTACAT 3180
 3181 TACAAGATTCTCACAAACAAACCCATGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA 3240
 3241 AGTTTGAGAGTAAAACGTAAAAATTATTTTGTGACTTTCTAAGAGAAAGAGTA 3300
 3301 TTGTTATGTTCTCTAACCTCTGTGATTACTACTTTAAGTGATATTCAATTAAACATT 3360
 3361 GCAAATTATTTATTTATTTAATTCTTTGAGATGGAGTCTGCTGTACCCAGG 3420
 3421 CTGGAGTGCAGTGGAGTGTCTCTGCTCACTGCAACCTCCGCCTCTGGGTTCAAGCGAT 3480
 3481 TCTCGTGCCTCAGCTTCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCGACTA 3540
 3541 ATTTTTTTTATTTAGTAGAGACGGGTTTACCATGTTGCCAGGTGGTATCAAAC 3600
 3601 TCC TGACCTCAAGAGATCCACTCGCCTGCCCTCCAAAGTGTGGGATTACAGGCTTGA 3660
 3661 GCCACCACGCCGGCTAAAACATTGCAAATTAAATGAGAGTTAAAATAAATAATG 3720
 3721 ACTGCCCTGTTCTGTTAGTATGTAATCCTCAGTTCTCACCTTGCACTGTCTGCC 3780
 3781 ACTTAGTTGGTTATAGTCATTAACCTGAATTGGTGTATAGCTAGACTTTAAAT 3840
 3841 TTAAAGTTCTACAAGGGGAGAAAAGTGTAAAATTAAATGTTCAAGGACTCAAGGACTG 3900
 3901 CTTCACTTCCAAGTCAGGTAGTAGTCATCTAGTTAGCCAAAGGACTCAAGGACTG 3960
 3961 AATTGTTAACATAAGGCTTTCTGTTCTGGGAGCCGACTTCATTAAATTCTCTA 4020
 4021 AAACCTGTATGTTAGAGTTAACAGACTTTCTCCTCTCCATGAGTTGTGAAAT 4080
 4081 TTAATGCACAACGCTGATGTGGCTAACAGTTATTTAAGAATTGTTAGAAATGCTGT 4140
 4141 TGCTTCAGGTCTTAAATCACTCAGCACTCCAATTCTAATCAAATTGGAGACTTA 4200
 4201 ACAGCATTTGTCGTGTTGAECTATAAAAGCACCGATCTTCATCTAATCCGCA 4260
 4261 AAAATTGATCATTTGCAAAGTCAAAATAGCCATATCCAATCTTCCCCCTCCAA 4320
 4321 GAGTTCTCAGTGTCTACATGTAGACTATTCTTTCTGTATAAAGTCACTCTAGGATT 4380
 4381 CAAGTCACCACTTATTTACATTTAGTCATGCAAAGATTCAAGTAGTTTGCAATAAGT 4440
 4441 ACTTATCTTATTTGTAATAATTAGTCTGCTGATCAAAGCATTGCTTAATTGAG 4500
 4501 AAC TGGTTTAGCATTACAAACTAAATTCCAGTTAATTAAATAGCTTATATTGCC 4560
 4561 TTCTGCTCACATTGGTTTCTCCCTGTCCTTGATTACGGGCTAAGGTAGGGTAAG 4620
 4621 AXGGGTGTAGTGTAGTGTATATAATGTGATTGGCCCTGTTGATTATGATATTGTTAT 4680
 4681 TTTGTTGTTATATTACATTTCAGTAGTTGTTTGTGTTCCATTAGGGGAT 4740
 4741 AAAATTGATTTGAACTATGAATGGAGACTACCGCCCCAGCATTAGTTCACATGATA 4800
 4801 TACCCCTTAAACCGAATCATTGTTATTTCTGATTACACAGGTGTTGAATGGGAAA 4860
 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTGCTGTAGAGAA 4920
 4921 ATGAAATAAAATGGGGCTGGGCTCAGGGCTCACGCCCTGTAATCCCAGCACTTGGGAGG 4980
 4981 CTGAGGCAGGTGGATCACGAGGTCAAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC 5040
 5041 CCCGTCTCTACTAAAAAACAGAAAATTAGCCGGCGTGGTGGCGGGCGCTGTAGTCCCA 5100
 5101 GCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTGA 5160
 5161 GCCGAGATCTGCCACTGCACTCCAGCCTGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220
 5221 AAAAAAAAAAG 5232

Fig. 1 (cont.)

SEQ. ID 5 - 1 TTGCTCTGTCACCCAGTTGGAGTGCAGTTATGCAGTCTCACACTGCAAGCTCTGCCCTCA 60
 61 TGGGCTCAAGTGAACCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACCACAGGCAGGTGCC 120
 121 ACCATGTCGGCTAATTTGAGTTCTTGTAGAGATGGTGTGTTGCCAAGTCACCCAG 180
 181 TTTGAGGCTGGTCTCAAACACCTGGGCTCAAGCAATCCATCTACCTCAGCCTCCAAAGT 240
 241 GCTGGGATTACAGGAGTGAGCCATGGCATAGGGCTTGTGGGGTGTCTTTAAATGAA 300
 301 AGCATACTCTGTTACGTATTTGATATGAAGGAATATCCTCCTTCCACAAAGACAAAA 360
 361 ATTATCCTATTTCTAAAACATATGTCCTTTCTACTTTCACTTTGTTACTTT 420
 421 TGATGGACACATGTGTTACATTGATTCACTTCTCATAAATTCTGCTGTAAGAAAACAA 480
 481 TAGTGCCAGTTCAATGACAATAGCAACAGTCTGTTATTGCTAGACTGTTACTGTTAGTG 540
 541 GAGACTACCAAGAACAGTCAGTCCCAGTGTAGGGAAATCAAAGAGAACATGTCCCTCT 600
 601 AAAGGGCACAGCTGCTCAGCTTAGCTGATTGCTGCCCTGCAGGACTATAGGCCAG 660
 661 TGTGCTAGATCTTGATGTTCAAGAGAAGCTGGAATCTAGAATGTGATGGGAAGTC 720
 721 TCTTACATTTAACATGTTGGCAATTATGGTAAGATTAAAAACTGTGTTCCAAGAA 780
 781 AAAAATGGATTTGGAACTGGATAATTCAAATGAGGCATGCAAGTAACTACAGCAT 840
 841 GGTACAATGTGAATTCTGGTTCTTAATTGCACTGTAATTAGGTAAGATGTTAGCTT 900
 901 TGGGAAAGCTAAGTCAGAGTATGCAAGAACTATTATTTGTAAGTTCTAAGTAT 960
 961 AAATAAATTCAAAATAAAACTAGTAAAGAACTATAATGCAATTCTATGTAA 1020
 1021 GCCAAACATAATATGTCCTCCAGTTGAAACCTCTGGGTTTATTTATTTATTTATT 1080
 1081 TTTGAGACAGAGTCTGCTGTGTCACCCAGGCTGGAGTGTAGTGGCACTATTGCGGCCA 1140
 1141 CTGCAACTCCACCTCCCAGGCTCAAATGATTCTCCTGCCTCAGCCTCCGGAGTAGCTGG 1200
 1201 GATTACAGGCGCGTACCAACACCCAGCTAATTTGTTATTTAGTAGAGATGGGGTT 1260
 1261 TCACCATTTGGCAGGCTGGTTGAACCTCCTGACCTCAAGTGATCCACTGTTGGC 1320
 1321 CTCCCCAAAATGCTGGGATTACAGCGTGAGCCACTGCAACAGGCTCTGTTTT 1380
 1381 TATCTCTTTGGCCTCTACAGTGCCTAGAAAGCACCTGATACTGGTAAACGATCAGT 1440
 1441 AATTACTAGTACTCTATTTGGAGAAAATGATTTTAAAGTCAATTGTTCCATCCA 1500
 1501 TGAGTCGTTGAGTTAAAACGTCTTTGTTGAAACAGGTTACAAAGGAG 1560
 1561 GAAAACGACTCTCTAGATTTTCAGTTCTCTATAAAATCAAACATCTCAAAA 1620
 1621 TGGAGACCTAAACCTTAAAGGGACTTAGTCTAACTCGGGAGGTAGTTGTGCATGG 1680
 1681 GTAAACAAATTAAAGTATTAACCTGGTGTACTATCCAAGAATGCTAATTATAAAACA 1740
 1741 TGATCGAGTTATATAAGGTATACCATATGAGTTGATTGAAATTGATTGTGAAAT 1800
 1801 AAAGGAAAAGTGTAGCTAGCTGGGCATATTGTTAAAGCATTTTCAGAGTTGGCCAG 1860
 1861 GCAGTCTCTACTGGCACATTCTCCATTATGAGAATAGTACCTGTTGG 1920
 1921 AAAGATTTAAAATGAGTGCAGTTATGGAACAAGAGCTAAATCAATCCACTGCA 1980
 1981 AATTAAAGAAACATGCAGATGAAAGTTGACACATAAAATCTACAGTGACAAG 2040
 2041 AAAAATCAAGAACAAAGCTTTGATATGTCAACAAATTAGAGGAAGTAAAAGATAA 2100
 2101 ATGTGATGATTGGTCAAGAAATTATCCAGTTATTCACAAGGCCACTGATATTAAACGT 2160
 2161 CAAAAAGTTGTTAAATGGGCTTACCGCTGAGAATGATGAGGATGAGAATGATGGTT 2220
 2221 GAAGGTTACATTTAGGAAATGAAGAAACTTAGAAAATTAAATATAAAAGACAGTGATGAAT 2280
 2281 ACAAAAGATTTATAACAATGTGAAATTGGCCAGGGAAAGGAATTATGAAGT 2340
 2341 TAGATACAATTACTTACCTTGAGGGAAATAATTGTTGGAATGAGATGTGATGTTCTC 2400
 2401 CTGCCACCTGGAAACAAAGCATTGAAAGTCTGAGTTGAAAAGCCAACGTCGTGAGATC 2460
 2461 CAGGAAACCATGCTGCAAACCACTGGTAAAAAAAAAAAAAAAAAGCCACAG 2520
 2521 TGACTTGCTTATTGGTCAATTGCTAGTATTATGACTCAGAACCTTTACTAATGGCTAG 2580
 2581 TAAATCATAATTGAGAAATTCTGAATTGACAAGGTCTGCTGTTGAAATGGTAAATT 2640
 2641 TATTATTTTTGTCATGATAAAATTCTGGTTCAAGGTATGCTATCCATGAAATAATT 2700
 2701 TGACCAAAACTAAATTGATGCAATTGATTATCCATCTAGCCTACAGATGGCATCTGGT 2760
 2761 AACTTTGACTGTTAAAAAATAACCACTATCAGAGTAGATTGATGTTGGCTTCAG 2820
 2821 AACATTTAGAAAACAAAAGTCAAAATGTTTCAAGGAGGTGATAAGTTGAATAACTC 2880
 2881 TACAATGTTAGTTCTTGAGGGGGACARAAAATTAAATCTTGAAAGGTCTTATT 2940
 2941 CAGCCATATCTAAATTATCTTAAGAAAATTGAAACAAAGGGAAATGAAATATATCATG 3000
 3001 ATTCTGTTTCCAAAAGTAACCTGAATATGCAATGAAGTTCACTGTTATTGGTAG 3060
 3061 TTTGGCAGAGTCTCTTTGAGCACCTGTTGCTACCATATAACAGAGGACATTCC 3120
 3121 ATGTTCTAGCCAAGTATACTATTAGAATAAARAAACTTAACATTGAGTTGCTTCAACAGC 3180

Fig. 2

3181 ATGAAACTGAGTCCAAAAGACCAAATGAACAAACACATTAACTCTGATTATTATTTA 3240
 3241 AATAGAATAATTAAATTGTGTAAGATCTAATAGTATCATTAACTTAAGCAATCATATTCC 3300
 3301 TGATGATCTATGGAAATAACTATTATTAATTAAATATTGAAACCAGGTTAACAGATGTG 3360
 3361 TTAGCCAGTCCTGTTACTAGTAATCTCTTATTGGAGAGAAATTAGATTGTTGT 3420
 3421 TCTCCTTATTAGAAGGATTGTAGAAAGAAAAATGACTAATTGGAGAAAATTGGGGAT 3480
 3481 ATATCATATTCACTGAATTCAAATGTCTCAGTGTAAATCTTACCAATTACCAATTACGT 3540
 3541 ACCTCTAAGAAATAAAAGTCTAATTAAATATGATGTCATTAATTATGAAATACTT 3600
 3601 CTTGATAACAGAAGTTAAAATGCCATCTTAGAATCAGTGAATATGGTAATGTATTA 3660
 3661 TTTCCCTCTTGAGTNAGGTCTGTGCTTTNTCCGGCACTAAATNTCACCATNT 3720
 3721 CCAANAAGCAAANTAAACCTATTCTGAATATTGGCTGTGAAACACTTGNCAAGCAGAGC 3780
 3781 TTTCCCNCCATGNNAAGCTCATGAGTCACACATTACATCTGGGGTGAATGC 3840
 3841 CACTGAAACATTCTAGTAGCCTGGAGNAGTTGACCTACCTGTGGAGATGCCATTA 3900
 3901 AATGGCATTCTGATGGCTTAATACACATCACTCTCTGTGNAGGGTTTAATTTCACA 3960
 3961 CAGCTTACTCTGTAGCATCATGTTACATTGTATGATAAGATTATACNAAGGTGCAAT 4020
 4021 TGTGTATTCTTCCTTAAATGTATCAGTATAGGATTAGAATCTCATGTTGAAACTCT 4080
 4081 AAATGCATAGAAATAAAATAATAAAATTTCATTGGCTTTCAGCCTAGTATTAA 4140
 4141 AACTGATAAAAGCAAAGCCATGCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCCTT 4200
 4201 TCTTCCCCATTCAATTGAAACATAGTAGAAAACAGCATATTCTTATCAAATTG 4260
 SEQ. ID 6-1 M N I V E N S I F L S N L M 14

 4261 TGAAAAGCGCCAACACGTTGAACTGAAATACGACTTGTATGTGAACTGTACCGAATGT 4320
 15 K S A N T F E L K Y D L S C E L Y R M S 34

 4321 CTACGTATTCCACTTTCTGCTGGGGTCTGTCTCAGAAAGGAGTCTGCTCGTGC 4380
 35 T Y S T F P A G V P V S E R S L A R A G 54

 4381 GTTTCTATTACACTGGTGTGAATGACAAGGTCAAATGCTCTGTTGTGGCTGATGCTGG 4440
 55 F Y Y T G V N D K V K C F C C G L M L D 74

 4441 ATAACCTGGAAAAGAGGGAGACAGTCCTACTGAAAAGCATAAAAGTTGTATCCTAGCTGCA 4500
 75 N W K R G D S P T E K H K K L Y P S C R 94

 4501 GATTGTTCAGAGTCTAAATTCCGTTAACAACTTGGAGCTACCTCTCAGCCTACTTTTC 4560
 95 F V Q S L N S V N N L E A T S Q P T F P 114

 4561 CTTCTTCAGTAACACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATT 4620
 115 S S V T H S T H S L L P G T E N S G Y F 134

 4621 TCCGTGGCTTATTCAAACCTCCATCAAATCCTGAAACTCCAGAGCAAATCAAGAAT 4680
 135 R G S Y S N S P S N P V N S R A N Q E F 154

 4681 TTTCTGCCTTGATGAGAAGTTCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTAC 4740
 155 S A L M R S S Y P C P M N N E N A R L L 174

 4741 TTACTTTTCAGACATGGCATTGACTTTCTGTCGCCAACAGATCTGGCACGGCAGGCT 4800
 175 T F Q T W P L T F L S P T D L A R A G F 194

 4801 TTACTACATAGGACCTGGAGACAGAGTGGCTTGCCTGTGGAAATTGAGCA 4860
 195 Y Y I G P G D R V A C F A C G G K L S N 214

 4861 ATTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGACATTCCCAAATGCCAT 4920
 215 W E P K D N A M S E H L R H F P K C P F 234

Fig. 2 (cont.)

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4921 TTATAGAAAATCAGCTTCAAGACACTTCAAGATAACAGTTCTAATCTGAGCATGCAGA 4980
235 I E N Q L Q D T S R Y T V S N L S M Q T 254

4981 CACATGCAGCCCGCTTAAACATTCTTAACGGCCCTCTAGTGTCTAGTTAACATCCTG 5040
255 H A A R F K T F F N W P S S V L V N P E 274
1 2

5041 AGCAGCTTCAAGTGCGGGTTTTATTATGTGG~~T~~AACAGTGTGATGTCAAATGCTTT 5100
275 Q L A S A G F Y Y V G N S D D V K C F C 294

5101 GCTGTGATGGTGGACTCAGGTGTGGAAATCTGGAGATGATCCATGGGTTAACATGCCA 5160
295 C D G G L R C W E S G D D D P W V Q H A K 314
2 3

5161 AGTGGTTTCCAAGGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTCATCCGTCAAG 5220
315 W F P R C E Y L I R I K G Q E F I R Q V 334
3 4

5221 TTCAAGCCAGTTACCCCTCATCTACTGAACAGCTGCTATCCACATCAGACAGCCCAGGAG 5280
335 Q A S Y P H L L E Q L L S T S D S P G D 354
4 5

5281 ATGAAAATGCAGAGTCATCAATTATCCATTGAAACCTGGAGAAGACCATTAGAAGATG 5340
355 E N A E S S I I H F E P G E D H S E D A 374

5341 CAATCATGATGAATACTCCTGTGATTAATGCTGCCGGAAATGGCTTAGTAGAAGCC 5400
375 I M M N T P V I N A A V E M G F S R S L 394

5401 TGGTAAAACAGACAGTCAGAGAAAAATCTAGCAACTGGAGAGAATTATAGACTAGTCA 5460
395 V K Q T V Q R K I L A T G E N Y R L V N 414

5461 ATGATCTTGTGTTAGACTTACTCAATGCAGAAGATGAAATAAGGGAAAGAGGAGAGAAA 5520
415 D L V L D L L N A E D E I R E E E R E R 434
5 6

5521 GAGCAACTGAGGAAAAAGAATCAAATGATTATTATTAATCCGGAAGAATAGAATGGCAC 5580
435 A T E E K E S N D L L I R K N R M A L 454

5581 TTTTCAACATTGACTTGTGTAATTCCAATCCTGGATAGTCTACTAACTGCCGGAAATTA 5640
455 F Q H L T C V I P I L D S L L T A G I I 474

5641 TTAATGAACAAGAACATGATGTTATTAAACAGAACAGACAGCTTTACAAGCAAGAG 5700
475 N E Q E H D V I K Q K T Q T S L Q A R E 494

5701 AACTGATTGATAACGATTTAGTAAAGGAAATTGCAAGCCACTGTATTAGAAACTCTC 5760
495 L I D T I L V K G N I A A T V F R N S L 514
6 7

5761 TGCAAGAAGCTGAAGCTGTGTTATGAGCATTATTGTGCAACAGGACATAAAATATA 5820
515 Q E A E A V L Y E H L F V Q Q D I K Y I 534
7 8

5821 TTCCCACAGAACAGATGTTCAGATCTACCAAGTGGAGAACATTGCGGAGACTACAAGAAG 5880
535 P T E D V S D L P V E E Q L R R L Q E E 554

5881 AAAGAACATGTAAGTGTATGGACAAAGAACAGTGTCCATAGTGTGTTATTCCGTGGTC 5940
555 R T C K V C M D K E V S I V F I P C G H 574

5941 ATCTAGTAGTATGCAAAGATTGTGCTCCTCTTAAGAAAGTGTCCCTATTGTAGGAGTA 6000
575 L V V C K D C A P S L R K C P I C R S T 594

Fig. 2 (cont.)

6001 CAATCAAGGGTACAGTCGTACATTCTTCATGAAGAAGAACAAAACATCGTCTAAC 6060
595 I K G T V R T F L S * 604

6061 TTTAGAATTAATTATAATGTATTATAACTTAACCTTATCCTAATTGGTTCCCTT 6120
6121 AAAATTTTATTATTACAACACTAAAAACATTGTTGTAACTATTTATATATGT 6180
6181 ATCTAAACCATATGAACATATATTAGAAACTAAGAGAATGATAGGCTTTGTTCTT 6240
6241 ATGAACGAAAAGAGGTAGCACTACAAACACAATTCAATCAAATTCAGCATTATTG 6300
6301 AAATTGTAAGTGAAGTAAAACCTTAAGATATTGAGTTAACCTTAAGAATTAAATATT 6360
6361 TTGGCATTGTACTAATAACCGGGAACATGAAGCCAGGTGTGGTATGTGCCCTGTAGTCC 6420
6421 CAGGCTGAGGCAAGAGAATTACTTGAGCCCAGGAGTTGAATCCATCCTGGGCAGCATAAC 6480
6481 TGAGACCCCTGCCTTAAAACAAACAGAACAAAACACCAGGGACACATTCTCT 6540
6541 GTCTTTTGATCAGTGTCTATAACATCGAAGGTGTGCATATATGTTGAATCACATTAA 6600
6601 GGGACATGGTGTAAAAAGAATTCTGTGAGAAAAAATTAAATAAGCAACCAAAAAA 6660
6661 AAAAAAAA 6669

Fig. 2 (cont.)

SEQ. ID 7 - 1 GAGCGCCCGGG¹⁻²CTGATCCGAGCCGAGCGGGCCGTATCCTTGTGGCGCCGCTGATTCC 60
 61 CGGCTCTGCCGAGGC²⁻³CTAGGCAGCCGAGCTCCGTGTTGCTGCCCGCCACTGC 120
 121 GATTACAACCC²⁻³CTGAAGAATCTCCCTATCCCTATTTGTCAGTAATAAAATCCC 180
 181 ATTATGGAGATCTGAAACTTATAAAGGGATATAGTTGAATTCTATGGAGTGTAAATT 240
 241 TGTGTATGAATTATTTAAAACATTGAAGAGTTTCAGAAAGAAGGCTAGTAGAGTT 300
 301 GATTACTGATACTTATGCTAACAGTACTTTGGTAGTACAATATTTGTTAGGCGT 360
 361 TTCTGATAACACTAGAAAGGACAAGTTATCTGTGATAAAATTGATTAATGTTACAC 420
 421 ATGACTGATAATTAGCTGAATAGTCCTAAATGATGAACAGGGTATTTAGTTTAAA 480
 481 TGCAGTGTAAGGTGTGCTGGAAATTATGGCTAACTAAGTTATGGAGAAAATAC 540
 541 CTTCAAGTTGATCAAGAATAATAGGGTACAAAGTTAGGAAGAAAGTCAACATGATGCT 600
 601 GCAGGAAATGGAAACAAATACAAATGATATTTAACAAAGATAGAGTTACAGTTTGAA 660
 661 CTTAAGCAAATTCAATTGACATCAAGCACTATAGCAGGCACAGGTTCAACAAAGCTTG 720
 721 TGGGTATTGACTTCCCCAAAAGTTGTCAGCTGAAGTAATTAGCCACTAAGTAAATA 780
 781 CTATGATGATAAGCTGTGAACTTAGCTTTAAATAGTGTGACCATATGAAGGTTTAA 840
 841 TTACTTTGTTATGGAATAAAATGAGATTTGGGTGTCATGTTAAAGTGTCTTATA 900
 901 GGGAAAGAAGCCTGCATATAATTTCACCTGTGGCATAATCAGTAATTGGTCTGTTAT 960
 961 TCAGGCTTCATAGCTGTAACCARATATAAAATAAAAGGCATAATTAGGTATTCTATAGT 1020
 1021 TGCTTAGAATTGTTAATATAAAATCTGTGAAAAATCAAGGAGTTTAAATTTCAG 1080
 1081 AAGTGCATCCACCTTCAGGGCTTAAGTTAGTATTAACTCAAGATTATGAACAAATAGC 1140
 1141 ACTTAGGTTACCTGAAAGAGTTACTACAACCCAAAGAGTTGTGTTCAAGTAGTATCTT 1200
 1201 GGTAATTCAAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAATCCAGTAAAGAA 1260
 1261 AGTGTAGTAAATTCTACATAAGAGTCTATGATTCTTTGGTAAAGATCTTAG 1320
 1321 TTCATGTGAAGAAATTTCATGTGAATGTTAGCTATCAAACAGTACTGTACCTACTCA 1380
 M 1
 1381 TGCAACAAACTGCCCTCCAAAGACTTTCCAGGTCCCTCGTATCAAAACATTAAGAGTA 1440
 SEQ. ID 8 - 2 H K T A S Q R L F P G P S Y Q N I K S I 21
 1441 TAATGGAAGATAGCACGATCTTGTCAAGATGGACAAACAGCAACAAACAAAAATGAAGT 1500
 1442 M E D S T I L S D W T N S N K Q K M K Y 41
 1501 ATGACTTTCTGTGAACCTACAGAATGTCTACATATTCAACTTCCCCGCCGGGTGC 1560
 1561 CTGTCTCAGAAAGGAGTCTGCTCGTGGTTTTATTATACTGGTGTGAATGACAAGG 1620
 1562 V S E R S L A R A G F Y Y T G V N D K V 81
 1621 TCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAACTAGGAGACAGTCCTATT 1680
 1682 K C F C C G L M L D N W K L G D S P I Q 101
 1681 AAAAGCATAAACAGCTATATCCTAGCTGTAGCTTATTCAAGAATCTGGTTCAAGCTAGTC 1740
 1682 K H K Q L Y P S C S F I Q N L V S A S L 121
 1741 TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTGCACATTCTATTCTC 1800
 1742 G S T S K N T S P M R N S F A H S L S P 141
 1801 CCACCTTGGAACATAGTAGCTTGTTCAGTGGTCTTACTCCAGCCTTCTCCAAACCTC 1860
 1862 T L E H S S L F S G S Y S S L S P N P L 161
 1861 TTAATTCTAGAGCAGTTGAAGACATCTCTCATCGAGGACTAACCCCTACAGTTATGCAA 1920
 1862 N S R A V E D I S S S R T N P Y S Y A M 181
 1921 TGAGTACTGAAGAACAGATTCTTACCATATGTGGCCATTAACTTTTGTCAC 1980
 1982 S T E E A R F L T Y H M W P L T F L S P 201

Fig. 3

9/33

1981 CATCAGAATTGGCAAGAGCTGGTTTATTATAGGACCTGGAGATAGGTAGCCTGCT 2040
202 S E L A R A G F Y Y I G P G D R V A C F 221

2041 TTGCCTGTGGTGGGAAGCTCAGTAACGGAAACCAAAGGATGATGCTATGTCAGAACACC 2100
222 A C G G K L S N W E P K D D A M S E H R 241

2101 GGAGGCATTTCCCAACTGTCCATTTGGAAAATTCTCTAGAAACTCTGAGGTTAGCA 2160
242 R H F P N C P F L E N S L E T L R F S I 261

2161 TTTCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTA
262 S N L S M Q T H A A R M R T F M Y W P S 281
3 4

2221 CTAGTGTCCAGTCAGCCTGAGCAGCTGCAAGTGCCTGGTTTATTATGTCAGCGCA 2280
282 S V P V Q P E Q L A S A G F Y Y V G R N 301

2281 ATGATGATGTCAAATGCTTTGTTGATGGTGGCTTGAGGTGTTGGAAATCTGGAGATG 2340
302 D D V K C F C C D G G L R C W E S G D D 321
4 5

2341 ATCCATGGGTAGAACATGCCAAGTGGTTCCAAGGTGTGAGTTCTGATA
322 P W V E H A K W F P R C E F L I R M K G 341
5 6

2401 GCCAAGAGTTGTTGATGAGATTCAAGGTAGATATCCTCATCTCTGAACAGCTGTTGT 2460
342 Q E F V D E I Q G R Y P H L L E Q L L S 361
6 7

2461 CAACTTCAGATACCAACTGGAGAAGAAAATGCTGACCCACCAATTATTCA
362 T S D T T G E E N A D P P I I H F G P G 381

2521 GAGAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTTAAATCTGCCTTG 2580
382 E S S S E D A V M M N T P V V K S A L E 401

2581 AAATGGGCTTTAATAGAGACCTGGTAAACAAACAGTTCAAAGTAAAATCCTGACA
402 M G F N R D L V K Q T V Q S K I L T T G 421

2641 GAGAGAACTATAAACAGTTAATGATATTGTCAGCACTCTTAATGCTGAAGATGAAA 2700
422 E N Y K T V N D I V S A L L N A E D E K 441
7 8

2701 AAAGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCA
442 R E E E K Q A E E M A S D D L S L I 461

2761 TTCGGAAGAACAGAACATGGCTCTTTCAACAATTGACATGTCAGCTCTATCCTGGATA 2820
462 R K N R M A L F Q Q L T C V L P I L D N 481

2821 ATCTTTAAAGGCCAATGTAATTAAATAAACAGGAACATGATATTATAAACAAAAACAC 2880
482 L L K A N V I N K Q E H D I I K Q K T Q 501

2881 AGATACCTTACAAGCGAGAGAACTGATTGATACCATTGGTAAAGGAAATGCTGCGG 2940
502 I P L Q A R E L I D T I L V K G N A A A 521

2941 CCAACATCTCAAAACTGTCTAAAGAAATTGACTCTACATTGTATAAGAACATTATTG 3000
522 N I F K N C L K E I D S T L Y K N L F V 541
8 9

3001 TGGAATAAGAATATGAAGTATATCCAAACAGAACAGATGTTCAAGGTCTGTC
542 D K N M K Y I P T E D V S G L S L E E Q 561
9 10

Fig. 3 (cont.)

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3061 AATTGAGGAGGTTGCAAGAAGAACGAAC TTGTAAAGTGTATGGACAAAGAAGTTCTG 3120
562 L R R L Q E E R T C K V C M D K E V S V 581

3121 TTGTATTTATTCCCTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCTCTCTAAGAA 3180
582 V F I P C G H L V V C Q E C A P S L R K 601

3181 AATGCCCTATTCAGGGTATAATCAAGGGTACTGTTGTACATTTCTCTTAAAGAA 3240
602 C P I C R G I I K G T V R T F L S * 618

3241 AAATAGTCTATATTTAACCTGCATAAAAAGGTCTTAAAATATTGTTGAACACTTGAAG 3300
3301 CCATCTAAAGTAAAAGGGATTATGAGTTTCATTAGTAACATTCAATTGTTCTAGTCT 3360
3361 GCTTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATTTAATCTTAAATCTG 3420
3421 TTTATTACAAGGGAAAGATTTATGTTGGTGAACTATATTAGTATGTATGTGTACCTAAG 3480
3481 GGAGTAGTGTCACTGCTTGTATGCATATTCAAGGAGTTACTGGATTGTTGTCTTTC 3540
3541 AGAAAGCTTGAATACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTGGAG 3600
3601 TTCATCAGAGTTATGGTGCCGAATTGTCTTGTGCTTTCACTGTGTGTTTAAATAAG 3660
3661 GATTTTCTCTTATTCTCCCCCTAGTTGTGAGAAACATCTCAATAAAGTGTCTTAAAA 3720
3721 AGAAAAAAAAA 3732

Fig. 3 (cont.)

SEQ. ID 9-1 ATTTTTAAATTGATGCATTAACATTCTAAACATTCTGTTTAAATAGTAAAATT 60
 61 GAACTTGCCTTGAATATGTAATGATTCAATTATAACAATTATGCATAGTCCTTAATAATC 120
 121 TGCAATTTCATGCTGCTTCATGTTTCTAATTAAATGACTTCACATGTTAACATT 180
 181 ATAATTTCATGCTCATAGTTCCATTAAATATAAAATGAATACTTAAGATCAGTAATT 240
 241 TGCTCTGTTGTTATATACTATTTCATCAAAAGACAAAATGGGACTGAGGTTGAGGC 300
 301 TCGTTGCTAAAGCACTTCCTAAATGCAAAGGCCATTGATGGATCCCTAGTACTTAT 360
 361 TTAAGTGAGAGAGAACAGGCTGGGGTAGGTCTGTTAGAGCATGTGTTGGCATTAT 420
 421 GTGAAGCCAAACACTAAAAAGGAGAACAAACAAAGCGCAGACTTAAACTCAAGTG 480
 481 GTTGGTAATGTACGACTCTACTGTTAGAATTAAATGTGCTTAGTTATTGTGCCATT 540
 541 ATTTTATGTCACTGGATAATATATTAGTGCTTAGTATCAGAAATAGTCCTTATGCT 600
 601 TTGTGTTTGAAGTCTTAATGCAATGTTCTTTCTAGAAAAGGTGGACAAGTCCTATT 660
 661 TTCCAGAGAAGATGACTTTAACAGTTGAAGGAACCTAGAACTTTGTACTTGCAGACA 720
 SEQ. ID 10-1 M T F N S F E G T R T F V L A D T 17

721 CCAATAAGGATGAAGAATTGTTAGAAGAGTTAACAGATTAAACATTGCTAACTTCC 780
 18 N K D E E F V E E F N R L K T F A N F P 37
 781 CAAGTAGTAGTCCTGTTCAGCATCAACATTGGCGCAGCTGGGTTCTTATACCGGTG 840
 38 S S S P V S A S T L A R A G F L Y T G E 57
 841 AAGGAGACACCGTGCAATGTTCAAGTTGTCATGCCAATAGATAGATGGCAGTGGAG 900
 58 G D T V Q C F S C H A A I D R W Q Y G D 77
 901 ACTCAGCTGTTGAAAGACACAGGAGAATATCCCACATTGCAAGATTCAATGGTTTT 960
 78 S A V G R H R R I S P N C R F I N G F Y 97
 961 ATTTGAAAATGGTGTGACAGTCTACAAATCCTGGTATCCAAATGCCAGTACAAT 1020
 98 F E N G A A Q S T N P G I Q N G Q Y K S 117
 1021 CTGAAAATGTGTGGAAATAGAAATCCTTGCACAGCTACTACACAGGCCACCTGAGACTCATG 1080
 118 E N C V G N R N P F A P D R P P E T H A 137
 1081 CTGATTATCTCTGAGAACTGGACAGGTTGTAGATATTCAGACACCATAACCGAGGA 1140
 138 D Y L L R T G Q V V D I S D T I Y P R N 157
 1141 ACCCTGCCATGTGTAGTAAGAAGCCAGATTGAAGTCATTCAGAACTGGCCGGACTATG 1200
 158 P A M C S E E A R L K S F Q N W P D Y A 177
 1201 CTCATTAAACCCCCAGAGAGTAGCTAGTGCTGGCCTACTACACAGGGCTGATGATC 1260
 178 H L T P R E L A S A G L Y Y T G A D D Q 197
 1261 AAGTGCATGCTTTGTTGGGGAAAATGAAAATGGAACCCCTGTGATCGTGCCT 1320
 198 V Q C F C C G G K L K N W E P C D R A W 217
 1321 GGTCAGAACACAGGAGACACTTCCAATTGCTTTGTTGGCCGGAACGTTAATG 1380
 218 S E H R R H F P N C F F V L G R N V N V 237
 1381 TTCGAAGTGAATCTGGTGTGAGTTCTGATAGGAATTCCAAATTCAACAAACTCTCAA 1440
 238 R S E S G V S S D R N F P N S T N S P R 257
 1441 GAAATCCAGCCATGGCAGAACATGAAAGCACGGATCGTTACTTTGAAACATGGACATCCT 1500
 258 N P A M A E Y E A R I V T F G T W T S S 277

Fig. 4

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1501 CAGTTAACAAAGGAGCAGCTTGCAGAGCTGGATTTATGCTTAGGTGAAGGCGATAAAG 1560
278 V N K E Q L A R A G F Y A L G E G D K V 297

1561 TGAAGTGCTTCCACTGTGGAGGAGGGCTACGGATTGGAAGCCAAGTGAAGACCCCTGGG 1620
298 K C F H C G G G L T D W K P S E D P W D 317

1621 ACCAGCATGCTAACGTGCTACCCAGGGTCAAATACCTATTGGATGAGAAGGGCAAGAAT 1680
318 Q H A K C Y P G C K Y L L D E K G Q E Y 337

1681 ATATAAAATAATATTCAATTAAACCCATCCACTTGAGGAATCTTGAGAAGAACTGCTGAAA 1740
338 I N N I H L T H P L E E S L G R T A E K 357

1741 AAACACCACCGCTAACAAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTCAAG 1800
358 T P P L T K K I D D T I F Q N P M V Q E 377

1801 AAGCTATAACGAATGGGATTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAAATCC 1860
378 A I R M G F S F K D L K K T M E E K I Q 397

1861 AAACATCCGGGAGCAGCTATCTACTTGAGGTCCCTGATTGCAGATCTTGAGTGCTC 1920
398 T S G S S Y L S L E V L I A D L V S A Q 417

1921 AGAAAGATAATACGGAGGATGAGTCAGTCAAACTTCATTGCAGAAAGACATTAGTACTG 1980
418 K D N T E D E S S Q T S L Q K D I S T E 437

1981 AAGAGCAGCTAACGGCCTACAAAGAGGAGAAGCTTCAAAATCTGTATGGATAGAAATA 2040
438 E Q L R R L Q E E K L S K I C M D R N I 457

2041 TTGCTATCGTTTTTTCTTGACATCTGCCACTTGTAAACAGTGTCCAGAAGCAG 2100
458 A I V F F P C G H L A T C K Q C A E A V 477

2101 TTGACAAATGTCCCAGTGTACACCGTCATTACGTCAACAAAAAATTATGTCTT 2160
478 D K C P M C Y T V I T F N Q K I F M S * 496

2161 AGTGGGGCACACATGTTATGTTCTTCTGCTCTAAATTGAATGTGTAAATGGAGCGAACT 2220

2221 TTAAGTAATCCTGCATTGCTTGCATTCCATTAGCATCCTGCTGTTCCAAATGGAGACCAATG 2280

2281 CTAACAGCACTGTTCCGTCTAACATTCAATTCTGGATCTTCGAGTTATCAGCTGTA 2340

2341 TCATTTAGCCAGTGTGTTACTCGATTGAAACCTTAGACAGAGAAGCATTATAGCTTT 2400

2401 CACATGTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGC 2460

2461 ATGTTCATGCCCTTGACATAAGCTAACAAATGGAGTGTCTGTATAAGCATGGAGATG 2520

2521 TGATGGAATCTGCCAATGACTTAATTGGCTTATTGTAACACGGAAAGAACTGCCCA 2580

2581 CGCTGCTGGAGGATAAAGATTGTTAGATGCTACTCTGTGTTTAGGATTCTGCC 2640

2641 ATTACTTGAATTATTGGAGTTATAATGTACTTATGATATTCCGAA 2691

Fig. 4 (cont.)

SEQ. ID 11 - 1 TGGGAGTTCCCCGGAGCCCTGGAGGAAGCACCGCAGGTCTGAGCAGCCCTGAGCCGGGC 60
 61 AGGGTGGGGCAGTGGCTAAGGCCAGCTGGGACGATTAAAGGTATCGGCCACCCAG 120
 121 CCACACCCCACAGGCCAGGGCAGGGTGCCACCCCCGGAGATCAGAGGTATTGCTGGCGT 180
¹₂ 181 TCAGAGCCTAGGAAGTGGCTGCGGTATCAGCCTAGCAGTAAAACCGACCAGAACCATG 240
 241 CACAAAACATCCCCAGAGAAAGACTTGTCCCTCCCTGTACATCTACCATGA 300
 301 ACATGGTTCAAGACAGGCCCTTAGCCAAGCTGATGAAGAGTGCTGACACCTTGAGT 360
 SEQ. ID 12 - 1 M V Q D S A F L A K L M K S A D T F E L 20
 361 TGAAGTATGACTTTCTGTGAGCTGTACCGATTGTCCACGTATTGCTTTCCAGGG 420
 21 K Y D F S C E L Y R L S T Y S A F P R G 40
 421 GAGTTCTGTGTAGAAAGGAGTCTGGCTCGTGGCTTTACTACACTGGTGCCAATG 480
 41 V P V S E R S L A R A G F Y Y T G A N D 60
 481 ACAAGGTCAAGTGTCTGCTGTGGCTGATGCTAGACAACGGAAACAAGGGGACAGTC 540
 61 K V K C F C C G L M L D N W K Q G D S P 80
 541 CCATGGAGAAGCACAGAAAGTGTACCCAGCTGCAACTTGTACAGACTTGAATCCAG 600
 81 M E K H R K L Y P S C N F V Q T L N P A 100
 601 CCAACAGTCTGGAAGCTAGTCCTCGGCCTTCTCTTCCACGGCGATGAGCACCATGC 660
 101 N S L E A S P R P S L P S T A M S T M P 120
 661 CTTTGAGCTTGCAAGTTCTGAGAATACTGGCTATTCTAGTGGCTTACTCGAGCTTC 720
 121 L S F A S S E N T G Y F S G S Y S S F P 140
 721 CCTCAGACCTGTGAACCTCGAGCAAATCAAGATTGTCTGCTTGGCACAAGTCCT 780
 141 S D P V N F R A N Q D C P A L S T S P Y 160
 781 ACCACTTGCAATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCATTGT 840
 161 H F A M N T E K A R L L T Y E T W P L S 180
 841 CTTTCTGTCAACAGCAAAGCTGGCAAAGCAGGCTTACTACATAGGACCTGGAGATA 900
 181 F L S P A K L A K A G F Y Y I G P G D R 200
 901 GAGTGGCCTGCTTGCCTGGCTGCGATGGAAACTGAGCAACTGGAACGTAAGGATGATGCTA 960
 201 V A C F A C D G K L S N W E R K D D A M 220
 961 TGTCAGAGCACCAAGAGGCATTCCCCAGCTGTCCGTTCTAAAGACTTGGGTCAAGTCTG 1020
 221 S E H Q R H F P S C P F L K D L G Q S A 240
 1021 CTTCGAGATACTGTCTCTAACCTGAGCATGCAGACACACGCAGCCGTATTAGAACAT 1080
 241 S R Y T V S N L S M Q T H A A R I R T F 260
 1081 TCTCTAACTGGCCTTAGTGCAGTGTCAAGTGTCTTGTGATGGTGGCTGAGGTGCT 1140
 261 S N W P S S A L V H S Q E L A S A G F Y 280
²₃ 1141 ATTATACAGGACACAGTGATGTCAAGTGTCTTGTGATGGTGGCTGAGGTGCT 1200
 281 Y T G H S D D V K C F C C D G G L R C W 300
³₄ 1201 GGGAACTGGAGATGACCCCTGGGTGAAACATGCCAAGTGGTTCCAAGGTGTGAGTACT 1260
 301 E S G D D P W V E H A K W F P R C E Y L 320

Fig. 5

1261 TGCTCAGAACAAAGGCCAAGAATTGTCAGCCAAGTCAAGCTGGCTATCCTCATCTAC 1320
 321 L R I K G Q E F V S Q V Q A G Y P H L L 340
 4 5
 1321 TTGAGCAGCTATTATCTACGTCAACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCG 1380
 341 E Q L L S T S D S P E D E N A D A A I V 360
 5 6
 1381 TGCATTTGGCCCTGGAGAAAGTCGGAAGATGTCGTATGATGAGCACGCCGTGGTTA 1440
 361 H F G P G E S S E D V V M M S T P V V K 380
 1441 AAGCAGCCTGGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTAGCGGCAGA 1500
 381 A A L E M G F S R S L V R Q T V Q R Q I 400
 1501 TCCTGGCCACTGGTGAGAACTACAGGACCGTCAGTGACCTCGTTAGGCTTACTCGATG 1560
 401 L A T G E N Y R T V S D L V I G L L D A 420
 6 7
 1561 CAGAAGACGAGATGAGAGAGGAGCAGATGGAGCAGGCCGGCCGAGGAGGAGTCAGATG 1620
 421 E D E M R E E Q M E Q A A E E E S D D 440
 1621 ATCTAGCACTAACCGGAAGAACAAAATGGTGCTTCCAACATTGACGTGTGTGACAC 1680
 441 L A L I R K N K M V L F Q H L T C V T P 460
 1681 CAATGCTGTATTGCCCTCTAACAGTCAAGGCCATCACTGAACAGGAGTGCATGCTGTGA 1740
 461 M L Y C L L S A R A I T E Q E C N A V K 480
 1741 AACAGAAACCACACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAGGAA 1800
 481 Q K P H T L Q A S T L I D T V L A K G N 500
 1801 ACACAGCAGAACCTCATTCAAGAAACTCCCTCGGGAAATTGACCCCTGCGTTACAGAG 1860
 501 T A A T S F R N S L R E I D P A L Y R D 520
 7 8
 1861 ATATATTGTGCAACAGGACATTAGGAGTCTCCCACAGATGACATTGCAGCTCTACCAA 1920
 521 I F V Q Q D I R S L P T D D I A A L P M 540
 8 9
 1921 TGGAAGAACAGTTGCCAACTCCAGGAGGAAAGAATGTGTAAAGTGTATGGACCGAG 1980
 541 E E Q L R K L Q E E R M C K V C M D R E 560
 1981 AGGTATCCATCGTGTCACTCCCTGTGGCCATCTGGCGTGTGCAAAGACTGCGCTCCCT 2040
 561 V S I V F I P C G H L V V C K D C A P S 580
 2041 CTCTGAGGAAGTGTCCATCTGTAGAGGGACCATCAAGGGCACAGTGCACATTCTCT 2100
 581 L R K C P I C R G T I K G T V R T F L S 600
 2101 CCTGAACAAGACTAACGGTCATGGCTGCAACTCAGCCAGGAGGAAGTCACTGTCACT 2160
 *
 2161 CCCAGCTCCATTGGAACTTGAGGCCAGCCTGGATAGCACGAGACACGCCAACACACA 2220
 2221 AATATAAACATGAAAAACTTTGTCTGAAGTCAGAAATGAATGAATTACTTATATAATAA 2280
 2281 TTTTAATTGGTTCTTAAAGTGTATTGCTTCAACTCAGAAATTGTTCTGTAA 2340
 2341 ACATATTACATACCTGCATCTAAAGTATTCAATATTCAATATTCAAGATGTGATG 2400
 2401 AGAGAGGGTTTGTCTGGCATTATGGTCAGAAACTAGAATCTCTCCGTTGCTTA 2460
 2461 GAAAGATTACAATGTGGCATTATGGTCAGAAACTAGAATCTCTCCGTTGCTTA 2520
 2521 AGAACCGGGAGCACAGATGTCCATGTGTTATGTATAGAAATTCTGTATTATTGGA 2580
 2581 TGACATTAGGGATATGAAATTATAAGAAATTGTGAGAAAAAGTTAATAAGCAA 2640
 2641 CATAATTACCTTTTTAAAGAAAAAAA 2676

Fig. 5 (cont.)

SEQ. ID 13-1 AGTTATATAAAATACGAAGTTCAAAAAGAAGGCTAGTCAACAGAAAAGCTTGCTAA 60
 61 AACAGATTCTTAGTTAGGTAACAAAAGAACCATGTCTGAATTGATTGATTGTTCT 120
 121 TAATTATAACAGACTTATAGTGGAAAGGGCCTTAAACACAGGGACTTTATAAAATGCA 180
 181 GTCTTAGGTTATGTGCAAATACTGTCGTTGACCAGATGTATTACATGATATATACA 240
 241 GAGTCAGGTGGTGTATAGAAGATTTAACAGTGAGGGAGTTAACAGTCTGTGCTTTAAG 300
 301 CGCAGTCCCTTACAGTGAATACTGTAGTCTTAATAGACCTGAGCTGACTGCTGCAGTG 360
 361 ATGTAACCCACTTATAGAGAATACTGTATGACATCTCTCTAAGGAAAACCAGCTGCAGAC 420
 421 TTCACTCAGTTCTTCATTCATAGGAAAAGGAGTAGTCAGATGTCATGTTAAGTCC 480
 481 TTATAAGGGAAAAGAGCCTGAATATATGCCCTAGTACCTAGGCTTCATAACTAGTAATAA 540
 541 GAAGTTAGTTATGGGAAATAGATCTCAGGTTACCCAGAAGAGTTCATGTGACCCCCAAA 600
 601 GAGTCCTAATCTAGTGTCTGGCAAGTGAGACAGATTGTCCTGTGAGGGTGTCAATTAC 660
 661 CAGTCCAAGCAGAACAGAACATGAATCTATCCAGTCAGGTGTCTGGTGGAGATCTAGTGT 720
 721 CCAAGTGGTGAGAAACTCATCTGGAAGTTAACCGGTAGAAATACTATTACTACTCAT 780
 1 M 1

781 GGACAAAATGTCTCCCAGAGACTCGGCCAAGGTACCTTACACCAAAAACCTAAACGTAT 840
 SEQ. ID 14-2 D K T V S Q R L G Q G T L H Q K L K R I 21

841 AATGGAGAAGAGGACAATCTTGTCAAATTGGACAAAGGAGAGCGAAGAAAAATGAAGTT 900
 22 M E K S T I L S N W T K E S E E K M K F 41

901 TGACTTTCTGTGAACCTACCGAATGTCTACATATTCACTTTCCAGGGGAGTTCC 960
 42 D F S C E L Y R M S T Y S A F P R G V P 61

961 TGTCTCAGAGAGGAGTCTGGCTCGTGGCTTTATTATACAGGTGTGAATGACAAAGT 1020
 62 V S E R S L A R A G F Y Y T G V N D K V 81

1021 CAAGTCTTCTGCTGTGGCTGATGTTGGATAACTGGAAACAAGGGACAGTCCTGTGA 1080
 82 K C F C C G L M L D N W K Q G D S P V E 101

1081 AAAGCACAGACAGTTCTATCCCAGCTGCAGCTTGTACAGACTCTGCTTCAGCCAGTCT 1140
 102 K H R Q F Y P S C S F V Q T L L S A S L 121

1141 GCAGTCTCCATCTAAGAATATGTCTCTGTGAAAAGTAGATTGCACATTGTCACCTCT 1200
 122 Q S P S K N M S P V K S R F A H S S P L 141

1201 GGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCCTCTTAATTCTAGAGCAGTGG 1260
 142 E R G G I H S N L C S S P L N S R A V E 161

1261 AGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCATGAGTACAGAACAGGCCAGATT 1320
 162 D F S S R M D P C S Y A M S T E E A R F 181

1321 TCTTACTTACAGTATGTGGCTTAAAGTTCTGTCAACCAGCAGAGCTGGCCAGAGCTGG 1380
 182 L T Y S M W P L S F L S P A E L A R A G 201

1381 CTTCTATTACATAGGGCTGGAGACAGGGTGGCCTGTTTGCCTGTGGTGGGAAACTGAG 1440
 202 F Y Y I G P G D R V A C F A C G G K L S 221

1441 CAACTGGAACCAAAGGATGATGCTATGTCAGAGCACCGCAGACATTTCCTACTGTCC 1500
 222 N W E P K D D A M S E H R R H F P H C P 241

1501 ATTTCTGGAAAATACCTCAGAAACACAGAGGTTAGTATATCAAATCTAAGTATGCAGAC 1560
 242 F L E N T S E T Q R F S I S N L S M Q T 261

Fig. 6

1561 ACACCTGCTCGATTGAGGACATTCTGACTGGCCACCTAGTGTCCCTGTTCAGCCCGA 1620
 262 H S A R L R T F L Y W P P S V P V Q P E 281

1621 GCAGCTTGCAAGTGTGGATTCTATTACGTGGATCGCAATGATGATGTCAAGTGCTTTG 1680
 282 Q L A S A G F Y Y V D R N D D V K C F C 301

1681 TTGTGATGGTGGCTTGAGATGTTGGAACCTGGAGATGACCCCTGGATAGAACACGCCAA 1740
 302 C D G G L R C W E P G D D P W I E H A K 321
 1 2

1741 ATGGTTCCAAGGTGTGAGTTCTTGATAACGGATGAAGGGTCAGGAGTTGTTGATGAGAT 1800
 322 W F P R C E F L I R M K G Q E F V D E I 341
 2 3

1801 TCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGGTCCACTTCAGACACCCCAGGAGA 1860
 342 Q A R Y P H L L E Q L L S T S D T P G E 361
 3 4

1861 AGAAAATGCTGACCCTACAGAGACAGTGGTGCATTTGGCCCTGGAGAAAGTCGAAAGA 1920
 362 E N A D P T E T V V H F G P G E S S K D 381

1921 TGTCGTCATGATGAGCACGCCGTGGTTAAAGCAGCCTGGAAATGGGCTTCAGTAGGAG 1980
 382 V V M M S T P V V K A A L E M G F S R S 401

1981 CCTGGTGAGACAGACGGTCAGCGGCAGATCCTGGCCACTGGTGGAGAACTACAGGACCGT 2040
 402 L V R Q T V Q R Q I L A T G E N Y R T V 421

2041 CAATGATATTGTCAGTACTTTGAATGCTGAAGATGAGAGAAAGAGAGAGGAGAAGGA 2100
 422 N D I V S V L L N A E D E R R E E K E 441
 4 5

2101 AAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACTGATTGGAGAAATAGAACGG 2160
 442 R Q T E E M A S G D L S L I R K N R M A 461

2161 CCTCTTCAACAGTTGACACATGTCCTTCTATCCTGGATAATCTTCTTGAGGCCAGTGT 2220
 462 L F Q Q L T H V L P I L D N L L E A S V 481

2221 AATTACAAAACAGGAACATGATATTATTAGACAGAAAACACAGATACCCCTACAAGCAAG 2280
 482 I T K Q E H D I I R Q K T Q I P L Q A R 501

2281 AGAGCTTATTGACACCGTTAGTCAGGGAAATGCTGCAGCCAAACATCTCAAAACTC 2340
 502 E L I D T V L V K G N A A A N I F K N S 521
 5 6

2341 TCTGAAGGAAATTGACTCCACGTTATATGAAAACCTTATTGTTGGAAAAGAATATGAAGTA 2400
 522 L K E I D S T L Y E N L F V E K N M K Y 541
 6 7

2401 TATTCCAACAGAACGACGTTCAAGGCTTGTGTCATTGGAAGAGCAGTGCAGGAGATTACAAGA 2460
 542 I P T E D V S G L S L E E Q L R R L Q E 561

2461 AGAACGAACTTGCAAAGTGTATGGACAGAGAGGTTCTATTGTTGTCATCCGTGTGG 2520
 562 E R T C K V C M D R E V S I V F I P C G 581

2521 TCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAGGAAGTGCCTCATCTGCAGGGG 2580
 582 H L V V C Q E C A P S L R K C P I C R G 601

2581 GACAATCAAGGGGACTGTGCCACATTCCTCATGAGTGAAGAATGGTCTGAAAGTATT 2640
 602 T I K G T V R T F L S * 612

Fig. 6 (cont.)

2641 GTTGGACATCAGAAGCTGTCAGAACAAAGAACATGAACTACTGATTTCAGCTCTTCAGCAGG 2700
2701 ACATTCTACTCTCTTCAAGATTAGTAATCTTGCTTATGAAGGGTAGCATTGTATATTT 2760
2761 AAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAGCTACAGGACTGTGCTGTTCC 2820
2821 AGAGCAGGAGTTGGGATGCTGCTGTATGTCCTTCAGGACTTCTGGATTGGAATTGT 2880
2881 GAAAGCTTGGATTTCAGGTGATGTGGAGCTCAGAAATCCTGAAACCAGTGGCTCTGGTAC 2940
2941 TCAGTAGTTAGGGTACCCCTGTGCTTCTGGTGCCTTCCTTCTGGAAAATAAGGATTTT 3000
3001 TCTGCTACTGGTAATATTTCTGTTGTGAGAAATATTAAGTGTTCCTTTAAAGG 3060
3061 CGTGCATCATTGTAGTGTGCAGGGATGTATGCAGGCAAAACACTGTGTATATAATAAAA 3120
3121 TAAATCTTTAAAAAGTGTAAAAAAAAAA 3151

Fig. 6 (cont.)

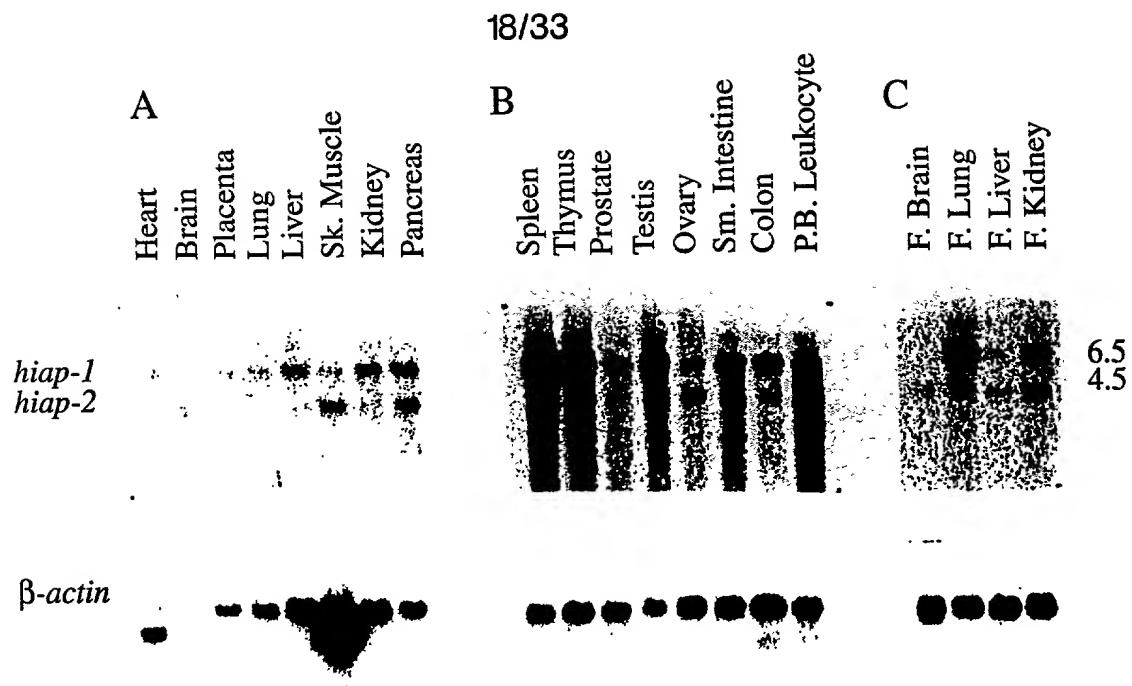


Fig. 7

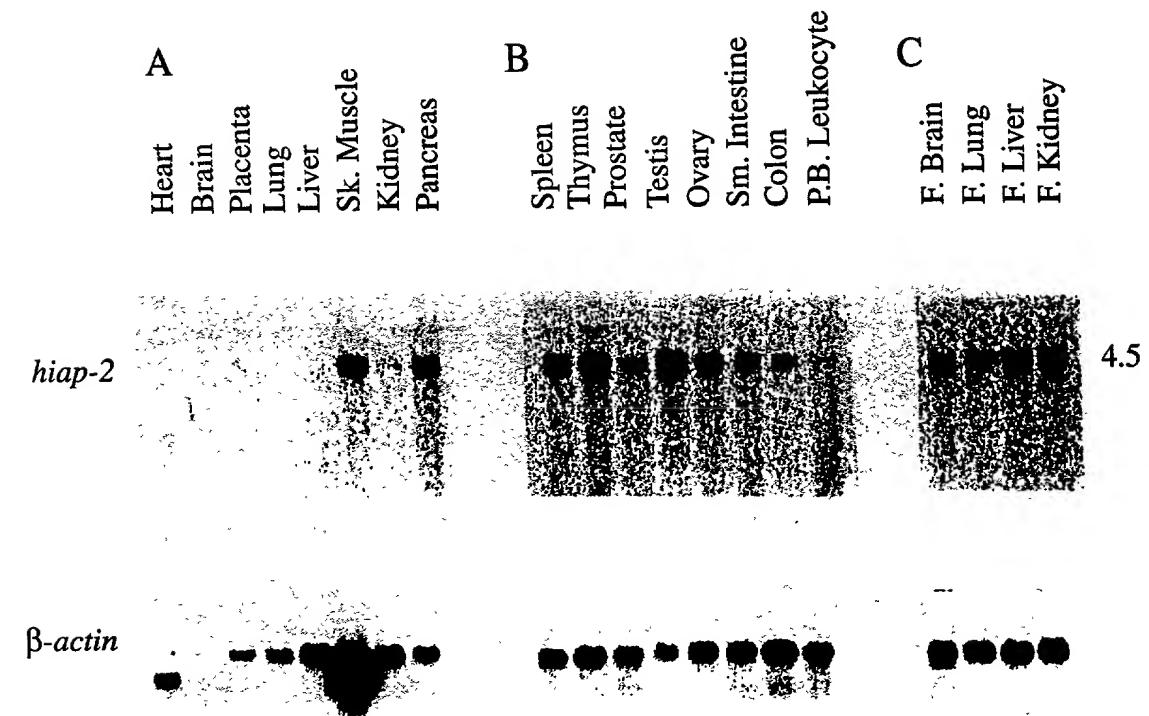


Fig. 8

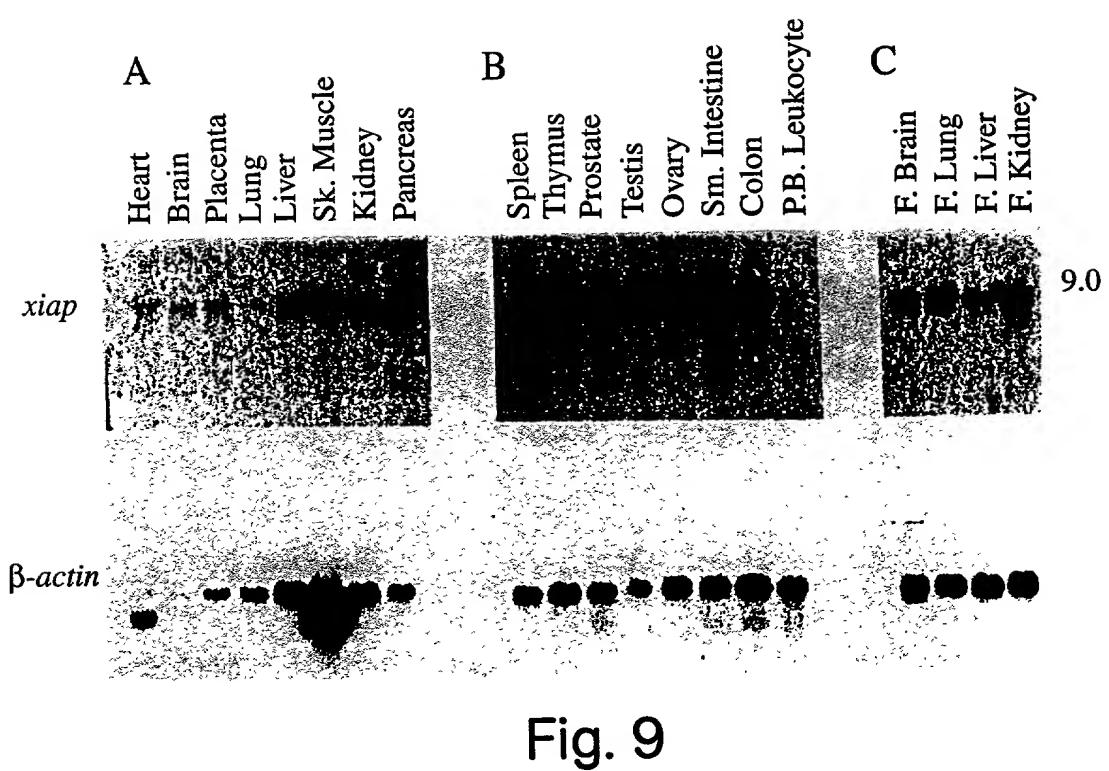


Fig. 9

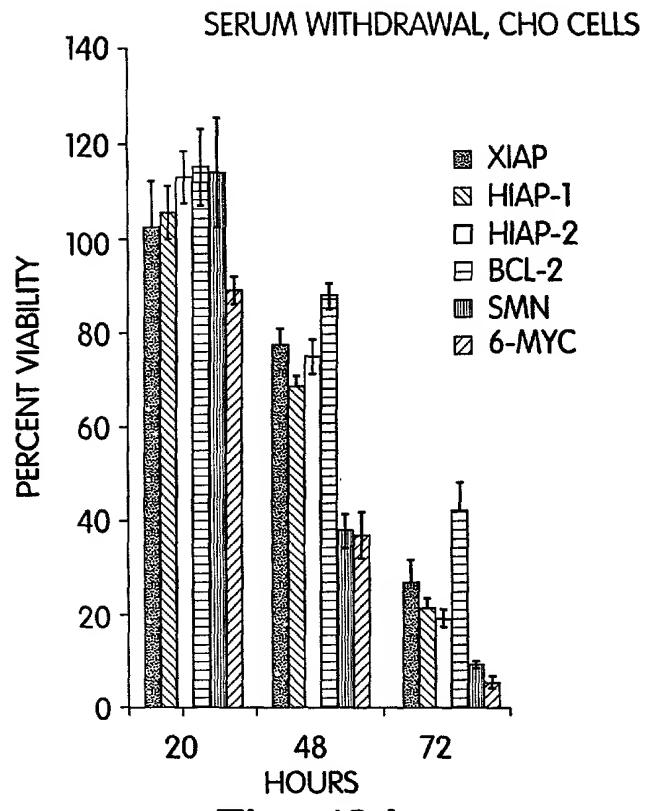


Fig. 10A

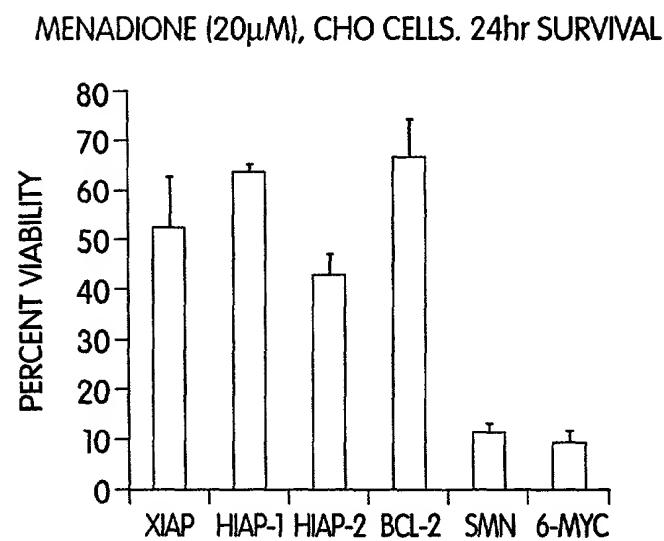


Fig. 10B

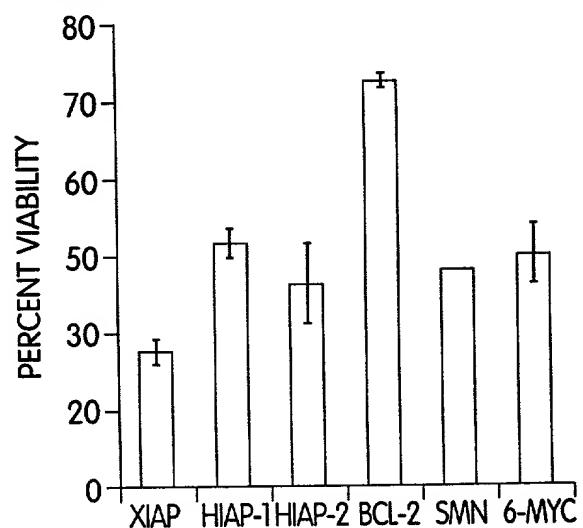
STAUROSPORINE (1 μ M), RAT-1 CELLS, 24 HOUR SURVIVAL

Fig. 10C

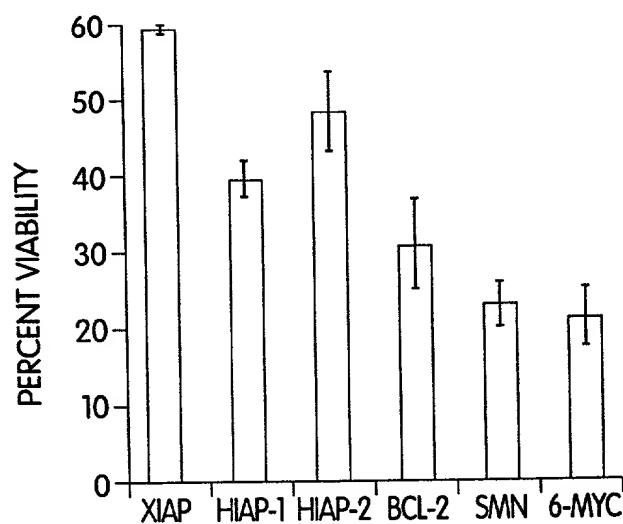
MENADIONE (10 μ M), RAT-1 CELLS, 18 HOUR SURVIVAL

Fig. 10D

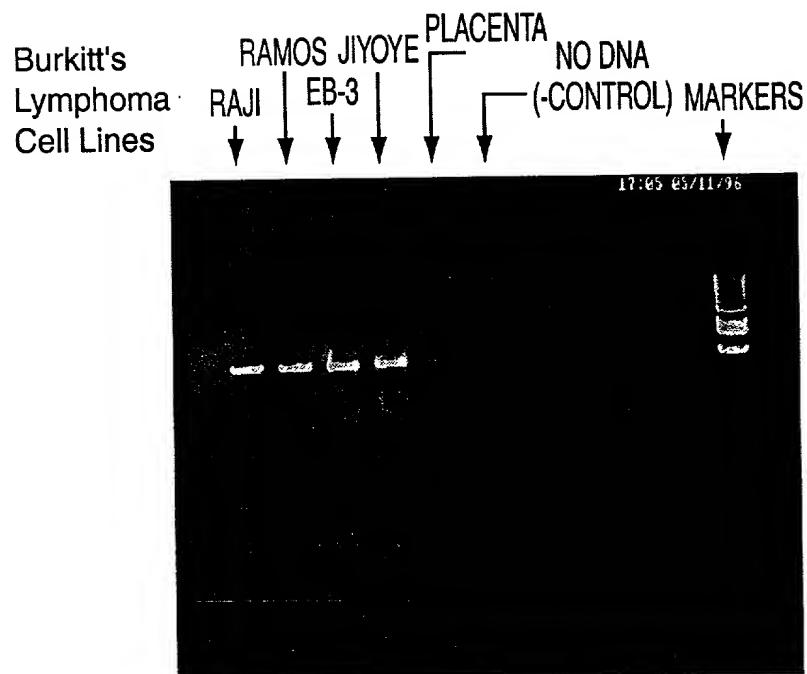


Fig. 11

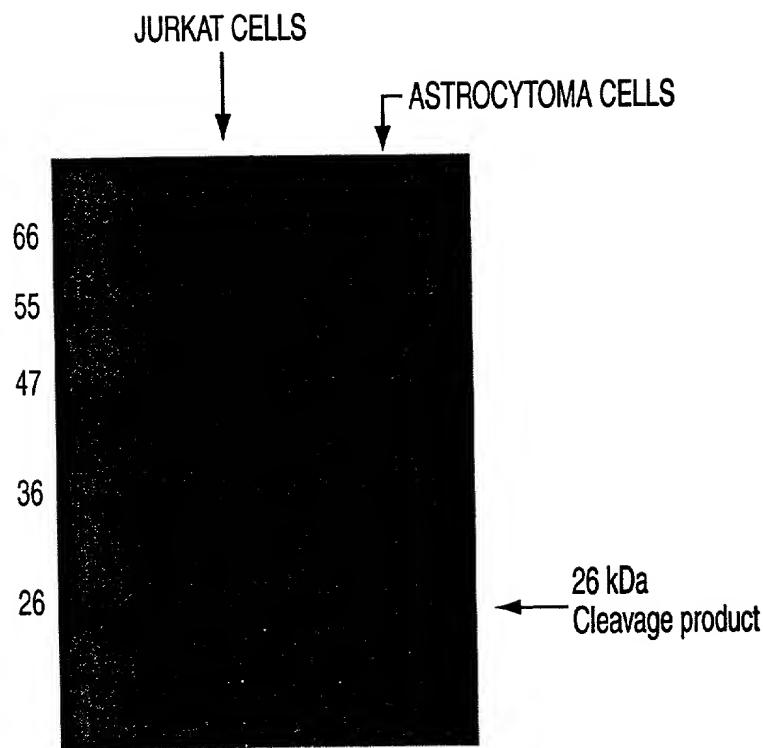


Fig. 12

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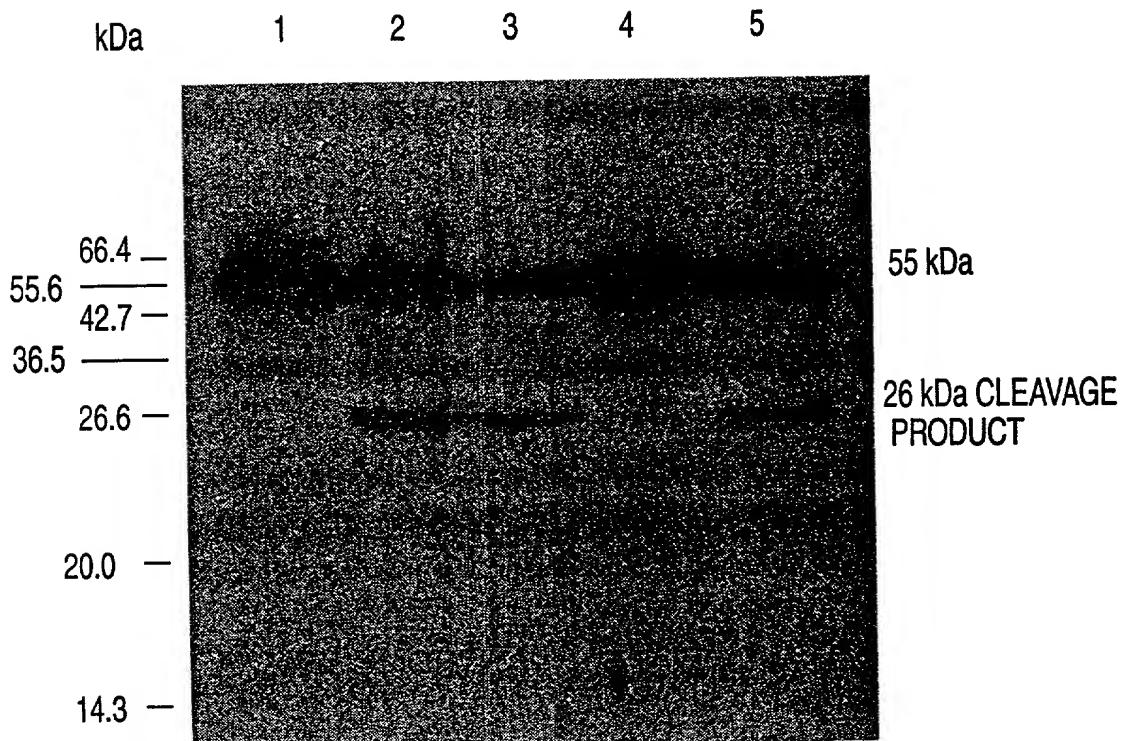


Fig. 13

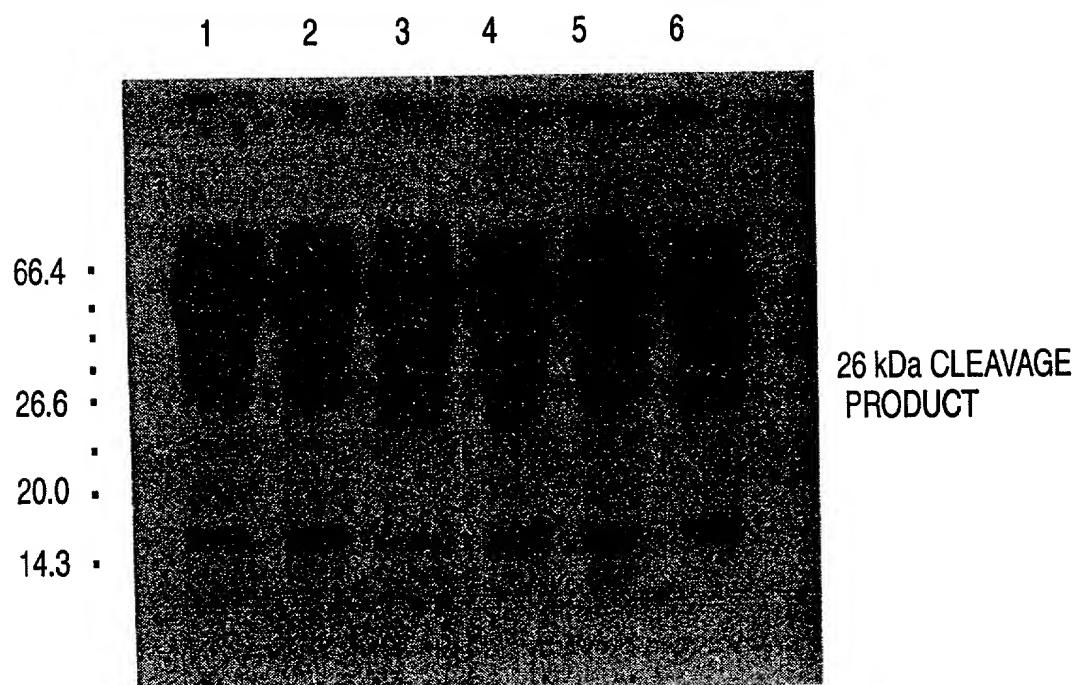
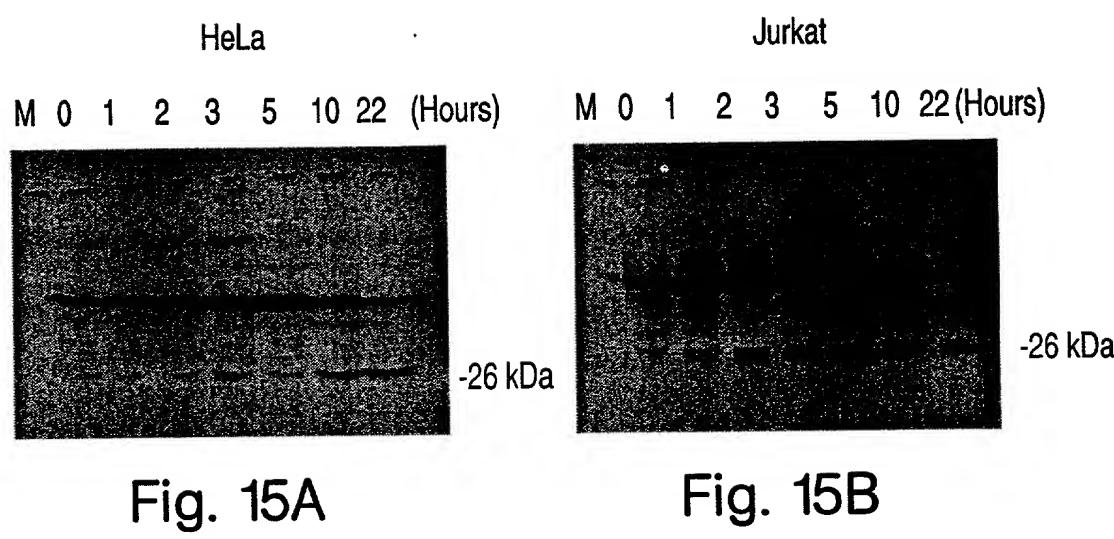


Fig. 14



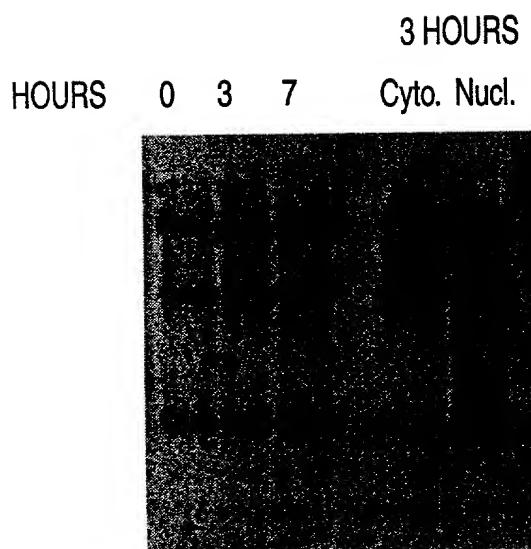


Fig. 16A

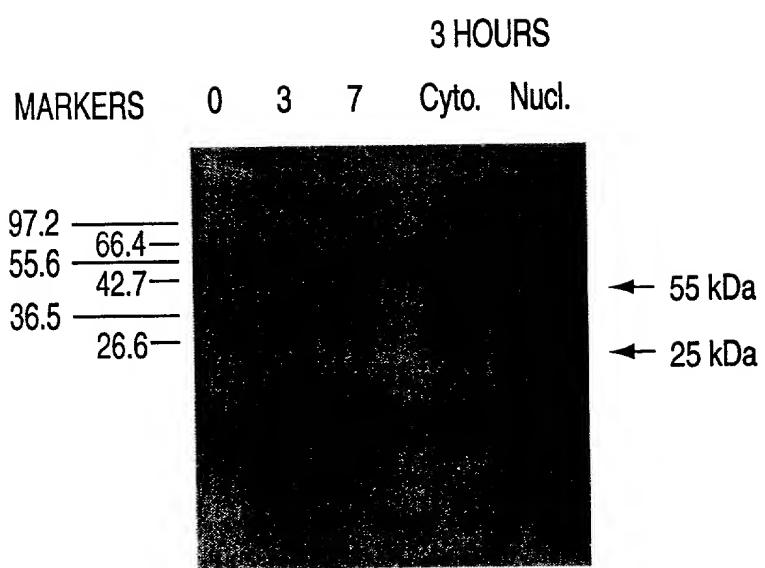


Fig. 16B

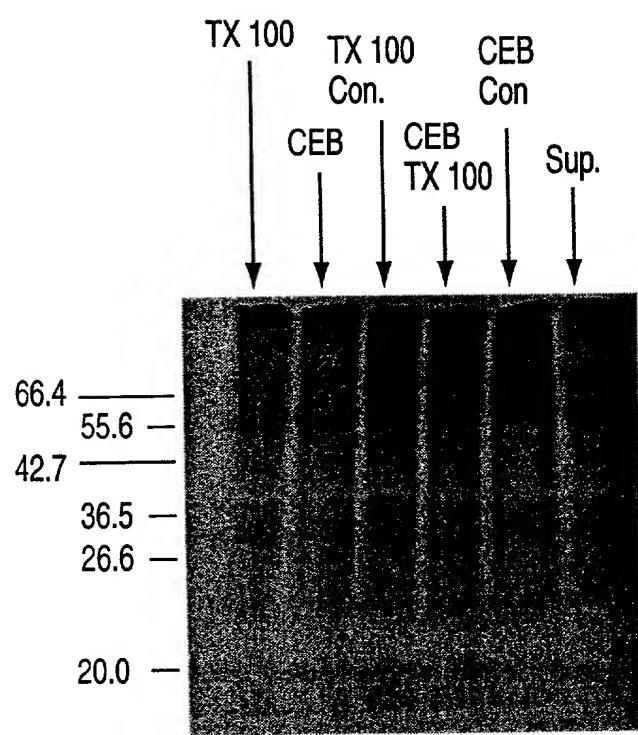


Fig. 17

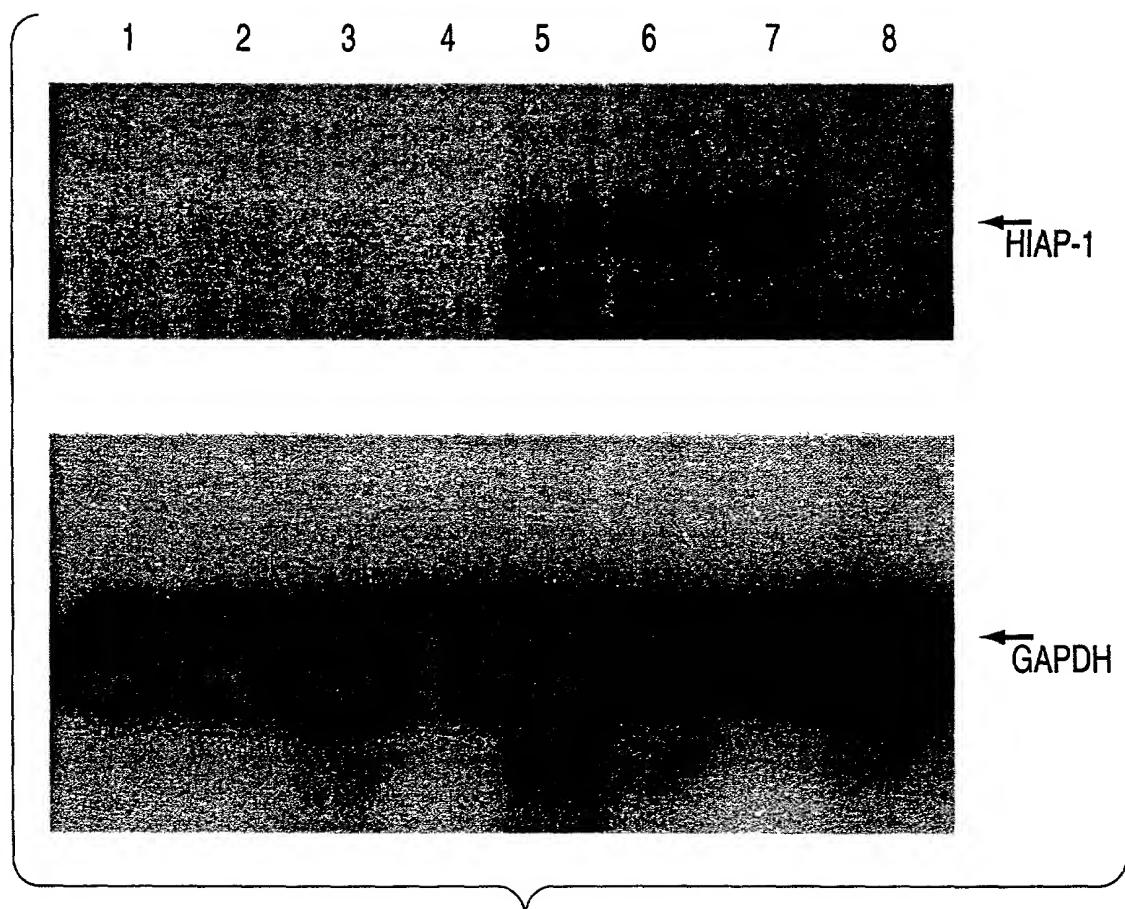
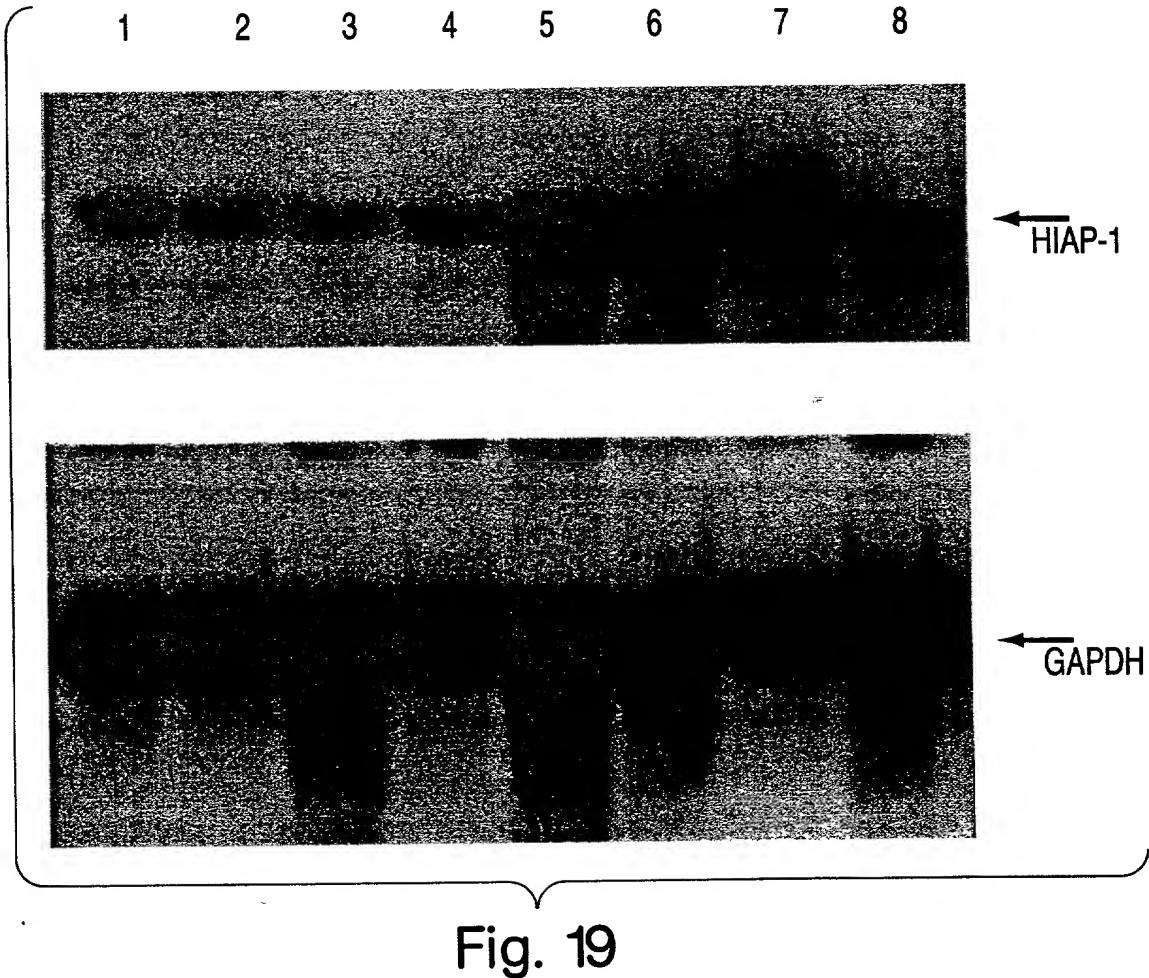
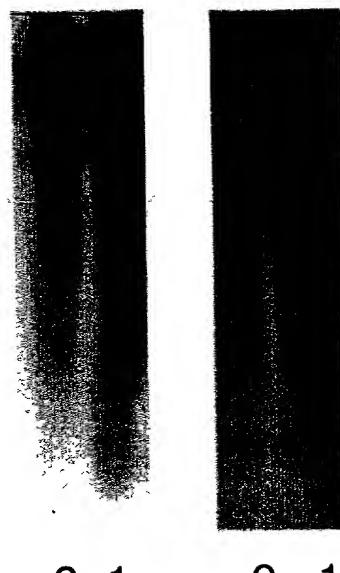


Fig. 18



C13 OV2008



TAXOL CONCENTRATION (μM)

Fig. 20

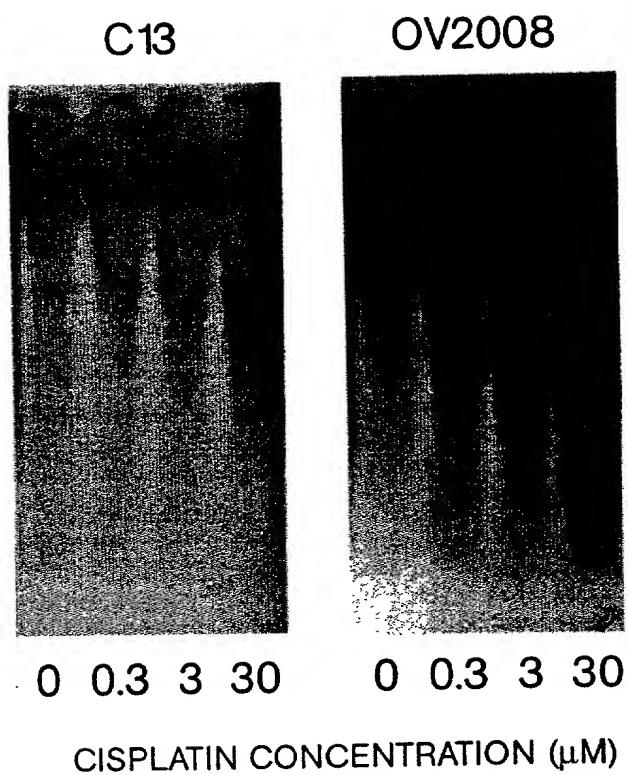


Fig. 21

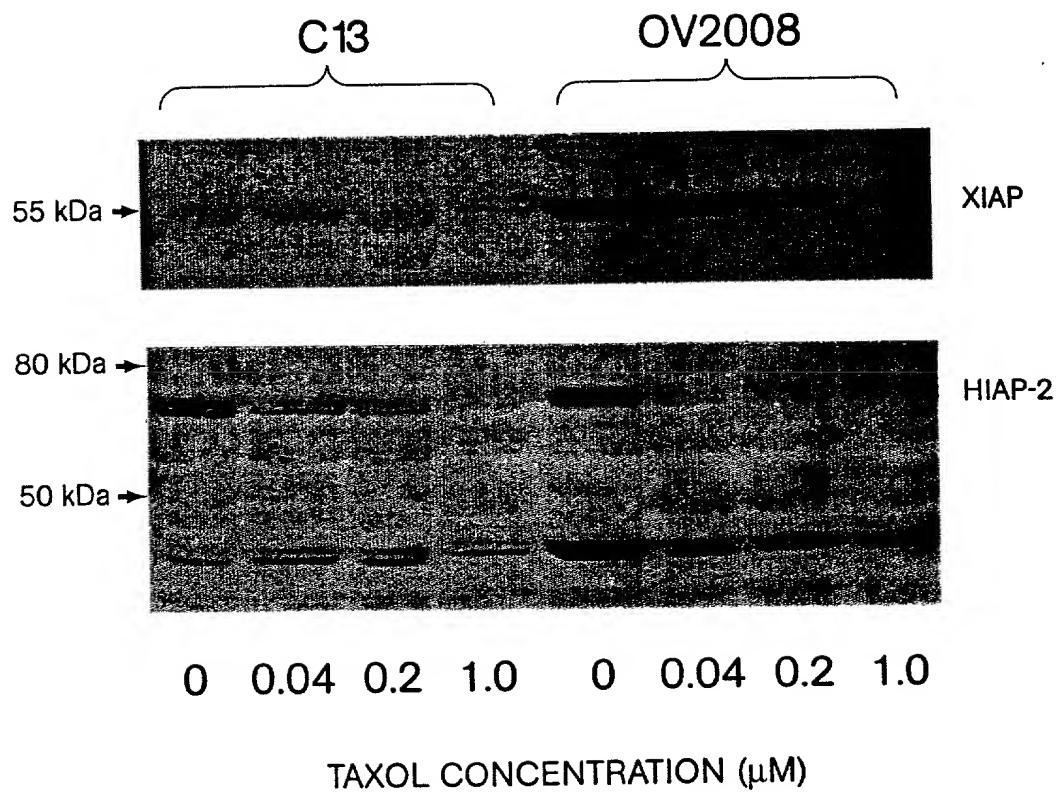


Fig. 22

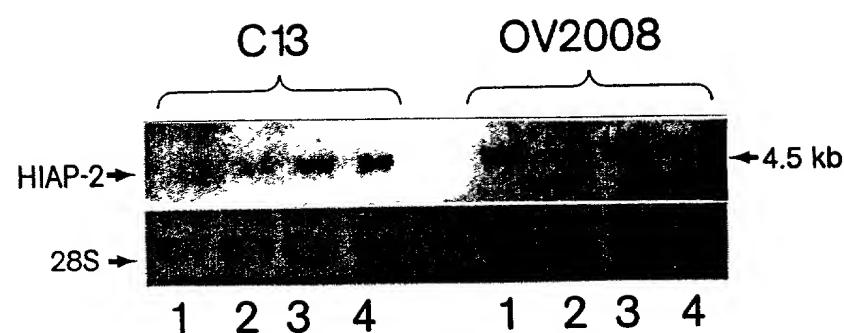


Fig. 23A

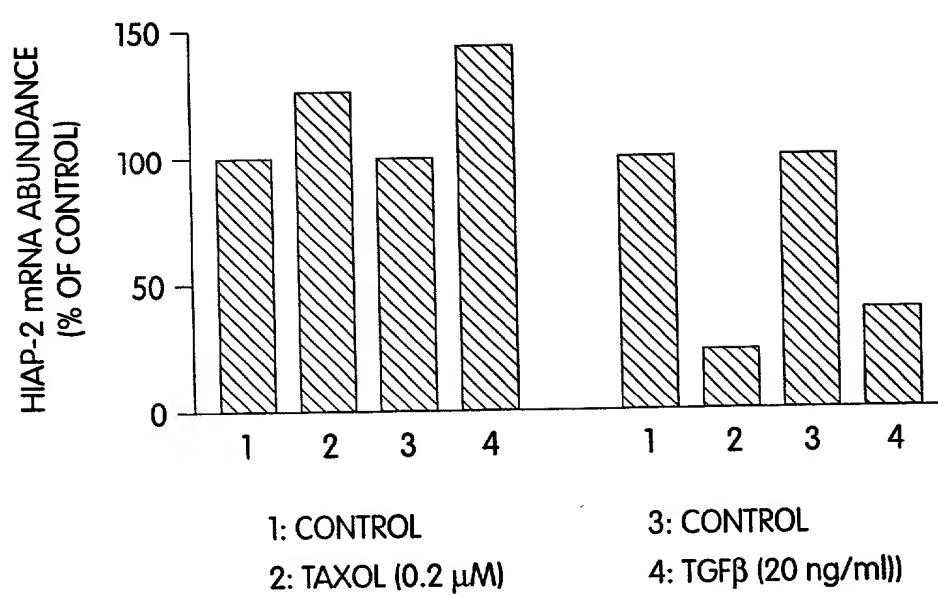


Fig. 23B

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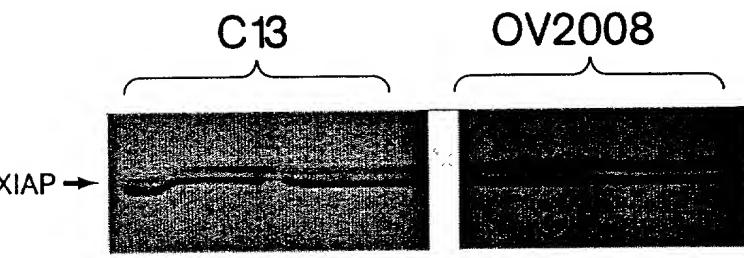


Fig. 24A

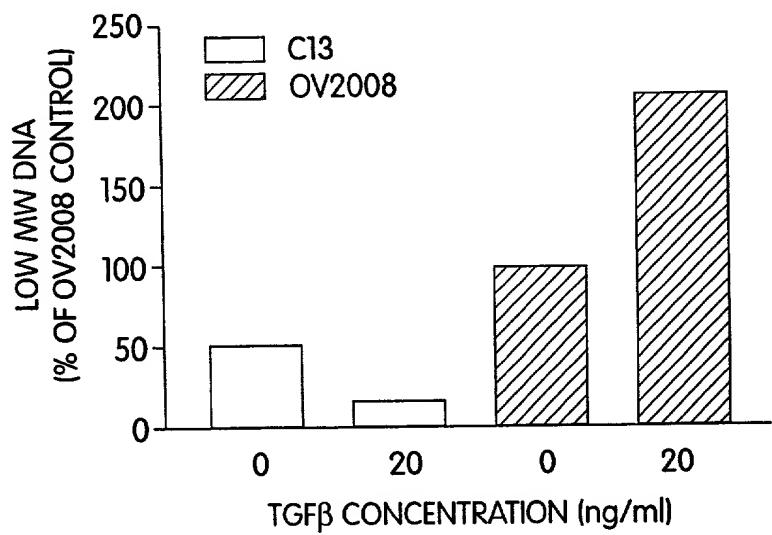


Fig. 24B